

No.	Score	Match	Length	DB	ID	Description
1	677.5	37.6	337	2	JG5832	neurotransmitter
2	529	29.4	387	2	S55550	5-HT4s receptor
3	529	29.4	406	2	S55549	serotonin 4 receptor
4	510.5	28.3	459	2	A56849	dopamine receptor
5	497.5	27.6	455	2	I51661	dopamine D1C receptor
6	493.5	27.4	353	2	I50475	dopamine D1 receptor
7	486	27.0	358	2	JQ1278	histamine H2 receptor
8	482	26.8	444	2	C55886	dopamine receptor
9	482	26.8	450	2	A55886	dopamine receptor
10	481	26.7	457	2	I51660	dopamine D1B receptor
11	480	26.7	451	2	I51659	dopamine D1A receptor
12	475	26.4	377	2	S68423	serotonin receptor
13	474	26.3	377	2	A53229	serotonin receptor
14	473	26.3	374	2	I77467	histamine H2 receptor
15	472.5	26.2	359	2	JH0449	histamine H2 receptor
16	467	25.9	446	2	I47217	dopamine receptor
17	466.5	25.9	377	2	B30341	G protein-coupled
18	466.5	25.9	386	2	S72168	dopamine receptor
19	462.5	25.7	463	2	B56849	dopamine receptor
20	461	25.6	483	2	A25896	beta-adrenergic receptor
21	459.5	25.5	359	2	JC4120	histamine H2 receptor
22	458	25.4	446	1	DYH0D1	dopamine receptor
23	454.5	25.2	477	1	DYH0D5	dopamine receptor
24	452	25.1	418	1	QRHYB2	beta-2-adrenergic
25	451	25.0	418	2	S10855	histamine H2 receptor
26	450.5	25.0	359	2	A39008	dopamine receptor
27	450	25.0	475	2	AI41271	beta-2-adrenergic
28	449.5	25.0	464	2	S12591	histamine H2 receptor
29	449	24.9	418	2	S50260	dopamine receptor

30	446.5	24.8	415	2	153040	beta-2 adrenergic
31	446.5	24.8	487	1	DPRD1	dopamine receptor
32	446	24.8	466	2	S36794	beta-1-adrenergic
33	438.5	24.3	413	1	QRHUB2	beta-2-adrenergic
34	437.5	24.3	466	2	B55886	dopamine receptor
35	433.5	24.1	477	1	QRHUB1	beta-1-adrenergic
36	432.5	24.0	366	2	A47321	serotonin receptor
37	429.5	23.8	428	2	A55042	beta-4C-adrenergic
38	429	23.8	480	2	153053	beta-1 adrenergic
39	427.5	23.7	366	2	S26048	serotonin receptor
40	427.5	23.7	386	2	A42688	serotonin receptor
41	427.5	23.7	386	2	S18637	serotonin receptor
42	427	23.7	477	2	S71323	alpha-1A adrenergic
43	425.5	23.6	429	2	S65656	alpha-1C-adrenergic
44	425.5	23.6	466	2	JN0765	alpha-1C-adrenergic
45	425.5	23.6	499	2	S65657	alpha-1C-adrenergic

## ALIGNMENTS

## RESULT 1

neurotransmitter receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Feb-1998 #sequence\_revision 13-Mar-1998 #seq\_change 24-Nov-1999  
C:Accession: J05832  
R:Zeng, Z.; Fan, P.; Rand, E.; Kyaw, H.; Su, K.; Madike, V.; Carter, K.C.; Li, Y.  
Biochem. Biophys. Res. Commun. 242, 575-578, 1998  
A:Title: Cloning of a putative human neurotransmitter receptor expressed in skeletal  
A:Reference number: J05832; MUID:9812534  
A:Accession: J05832  
A:Molecule type: mRNA  
A:Residues: 1-337 <GEN>  
A:Cross-references: CB:AF021818; NID:g2465431; PIDN:AA039581.1; PID:g2465432  
A:Experimental source: brain  
C:Genetics:  
A:Map position: 6q23  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; receptor; transmembrane protein  
F:29-63/Domain: transmembrane #status predicted <TM1>  
F:69-95/Domain: transmembrane #status predicted <TM2>  
F:114-118/Domain: transmembrane #status predicted <TM3>  
F:149-173/Domain: transmembrane #status predicted <TM4>  
F:186-200/Domain: transmembrane #status predicted <TM5>  
F:204-229/Domain: transmembrane #status predicted <TM6>  
F:253-310/Domain: transmembrane #status predicted <TM7>  
F:21/Binding site: carboxylate (asn) (covalent) #status predicted

Query Match	Score	DB 2;	length
37.68;	677.5;		337;
30.08;			
Best Local Similarity			

Matches 130; Conservative 67; Mismatches 125; Indels 11; Gaps 4

QY 3 FCHNININISCVKNNWSNDVRASLSKSLMWLILITLLVGNLIVIVSISISFVQLHTPTNNLTH 62  
 16 ECYQ-VNGSGDPRVTHTTIGTIVITVTCAGAGMTITIVGAGVAAEAVSGEVALITHTTETTTTIT 74AAGT

QY 63 SMATVDFLLGCLVMPYSMVRSAEHCWYEGVEVCKIHTSTIDIMLSSASIFHLFSISIDRY 12

123 AVCDPLRKAKMNLIVICWIFISWSVPAVFAFGMIFLEINFKGAEIYYKHVHCRGGS 18

Db 135 AICDPLEYPSKFTVRAVAIRYLAGWGVEPAAYTSLFLYTDVETRLSQ<sup>19</sup>WLEEMPCVSSQ<sup>19</sup>

[illegible]

243 SKERKAVTLGIVMGVELICWCPFFICTVMDPFLHIIPTLNTLVLYRGYLNSTNPMV 30  
OY  
245 KHERKAKTIGIVGTIYLICIPIETIDTMVDSDIHETMBDVEQIFWEFAVENSCANDIT 20



```

OY      201  PGTSMLCVYVYITVLIARQARLI-----SDANQKIQIGLEMNNGISQSER 246
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      207  PVAIMIVYITVITVIAKQKIRISALEKAAESAQNRRHSSMGNSLSMSESCSFKMSFKRET 266
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      247  KAVYTLGIVMGVFLICMCPPFICTVMDPEFLHY-----IIPPLNDVLIWFGYLNSTFN 299
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      267  KVLTLTSLIVMGVFLVOCMKLFFFLINOMVFCFCEADDTTDEPCISSTTFEDVFVWFGMANSSLN 326
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      300  PMVYAFEYPMERKALKMKML 318
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      327  PIYAFNAD-ERKAFSILL 344
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      5
151661
dopamine D1C receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
R:Accession: 151661
R:Sugamori, K.S.; Demchishyn, L.L.; Chung, M.H.; Miznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: 151659; MUID:95024150
A:Accession: 151661
A:Status: preliminary; translated from GR/EMBL/DBDB
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:Cross-references: EMBL:U07865; NID:g559763; PIDN:AAA50830.1; PID:g559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query March 1997: 27.6% Score 497.5; DB 2: Length 465;
Best Local Similarity 34.5%: Pred. No. 4.5e-34;
Matches 118; Conservative 61; Mismatches 130; Indels 33; Gaps 8;

QY 6 NIINISCVKNMNSND-----VRASLYSLMVLIIITTEVGNLIVIVSISHPKQLHTP 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 SIFNTV--NWVHADLDGNSDSLRLALGLLSLLISLLITLGNLVLCVAKFKFHLRSK 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 -TNWLIHSMATVDFLLGCLVMPYSNVRSAHCWYFGEWFECKIHTSTDIMLSASIFHLSF 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 VTNFVVISLAVSDELVALLVMPKAVTEVAGFWVGFD-FCDTWVAFDIMCSPTASILNLCI 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 ISIDRYACDPLRKAKANNILVTCMFISNRSVAVRAFGFIETLNFKGADEIYKYH 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 ISLDRYMAIASPFREKRTQVAFIMGVAMTLLISLISFIVQLSWHSRSHADELNVG 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 HORGCCSVFFKSISGVLPFTMSFIYPGSIMLCVYRIYLAKQRLISDAN-----OK 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 NITENCDSLSNTFYAISSLSIFIPVIMIGYIRIKYIAQTQIRRLSSLERAVEHAOR 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 IQIGLEKMGKGISQ--KEKAVKTLGIYGVFLICMCPFICTVMDPFLHYIIP----- 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 CSSRLSNEKSLTSRKEKRYLKLTSIIMGVYFPCMLPFFVLNCLMPCFHMMLPGQNEP 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 -----PTLNDVLIWFGYLNSTFNPVYAFEPYPMFRKALKML 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 PCVSETTFENIFWFGMANSSLNPIVYAFNAD-FRKAFPTIL 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
150475
dopamine D1 receptor - goldfish
C.Species: Carassius auratus (goldfish)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C.Accession: 150475
R.Fall, D.E.; Manelli, A.M.; Witte, D.G.; Lin, C.W.; Steffey, M.E.; Mackenzie, R.G.
Mol. Pharmacol. 44, 1113-1118, 1993
A.Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish
A.Reference number: 150475; MUID:94088471
A.Accession: 150475

```

A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: DNA  
A: Residues: 1-363 <PRA>  
A: Cross-references: GB:108602; NID: g212949; PIDN: AAA16322.1; PID: g212950  
A: Superfamily: vertebrate rhodopsin  
C: Keywords: neurotransmitter receptor

Query Match	27.4%	Score 493.5	DB 2	Length 363
Best Local Similarity	36.3%	Pred. No. 7.6e-34		
Matches 118; Conservative	59;	Mismatches 117;		Indels 31; Gaps 8;

```

0y 21 VRASLYSLMVLIIITLTVGNILIVYSVSHFQOLTP-TNNLIHSMGVDFLLQCLAMPVS 79
   || : : : ||| : || : : : || : : : || : : : || : : : || : : : || : : : ||
Db 23 VRVLGLGCLSLVLIIITLSTLGNLTQVCAATKFRHLNSKVTNFEVLSLAVSDLLVALVMPMK 82

0y 80 MYRSACHEWYGEVFPCKITHSTDMLSASFSHLSFISIDRYAAVCDPLKXKKNMILY 139
Db 83 ATEVAGFMFPG-AECDIMAFEDIMCSATSLNLCVSHVDYRWAISSPEFERKEMPRRA 141

0y 140 CMWIFISMSVPAVAFGMIPELNFPGAEELYYKHHVC-----RGCSVFEKISGVLT 193
Db 142 FWMIGANTLTSVLISF--IPVQLMKHKAQPIGFLVNAASRDLPDTCDDSSLNRTYAISS 199

0y 194 FMTSTYFGSITMLCYNYRIYLAEDQARLIS---DAWQKQI-----GLEMKNG 239
Db 200 SLISFYIPVAMIVYYQIYIRIADQKQIRRIISALERAESAQIRHDSGSGSNMDDLESFK 259

0y 240 ISOSKERKAVATLGIWGVGFLIQCPEFICTVMDPFLAHY-----ITPPTLNDVLIMFGY 293
Db 260 LSKRETVLAKTLISIMGVFQCMPLPEILLNCVYPCFKRTSNGLPICSPITTFDVFVFWG 319

```

```

RESULT 7
histamine H2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: J01278
R:Ruat, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 179, 1470-1478, 1991
A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.
A:Reference number: J01278; MUID:92028890
A:Accession: J01278
A:Molecule type: DNA
A:Residues: 1-358 <RU>
A:Cross-references: GB:557565; MID:9236183; PIDN:AAH19935.1; PID:9236184
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane P
F:22-45/Domain: transmembrane #status predicted <TM1>
F:58-81/Domain: transmembrane #status predicted <TM2>
F:93-113/Domain: transmembrane #status predicted <TM3>
F:136-159/Domain: transmembrane #status predicted <TM4>
F:178-203/Domain: transmembrane #status predicted <TM5>
F:234-260/Domain: transmembrane #status predicted <TM6>
F:267-288/Domain: transmembrane #status predicted <TM7>
F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:220.311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 27.0% Score 486; DB 2: Length 358;
Best Local Similarity 34.0% Pred No.3.2e-33;
Matches 117; Conservative 56; Mismatches 123; Indels 48; Gaps 7;

11 SCVKNMSNDVRASLSTLWVLIITFLVGNLIYVSIHFQKQLHPTNMLHSMATVDFL 70
11 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 9 SCCLDSMLAKVTISV--VLTFLILITAGVNVVCAVSLNRRILRSITNCFVLSLATDIL 66
71 LGLVWPYISNVAEHCWTFGEVEFCIKHSTDMILSSAIFHLSPISIDRYVAVDPLRY 130

```

```

Db 67 IGLVLPESAIVQISFTWSFGHVCNITYISLDVMTCTASINLEMISIDRYACVADPLKY 126
Qy 131 KAKMNLIVICVMIFISMSVPAVAFGMIFLELNFGKAEIYYKHVHCRG-----CSVFF 185
Db 127 PVLVFPVRAISLVITWISITLSLSTHLMGNSRNG-----TRGNDTPFKQGV 177
Qy 186 SKISGVLFPMISFYIPGSIIMLCVYRIYILIAKEQARLISDANOKIOLGEMKNGISQSK- 244
Db 178 NEVYGLVIGLVTFYLPILMICYTYRIEFKIAREQAKRI-----NHISWKA 223
Qy 245 -----ERKAKVTGIYMGVFLICMCPFFICTVMDPLHY-----IIPPLNDVLIHFGY 293
Db 224 ATRERHAKVTILAAVAGAFICMFPFTAFV-----YGLGSDAIDNAEGIVMLGY 277
Qy 294 INSTENPMVYAFEPYFWRKALMKMLFGKIFORDSSRCKLFEELS 337
Db 278 AASALNPILYALNDRFRTAYOQLFHCKRFASHNSHRTSLRNN 321

```

```

RESULT 8
C55886
dopamine receptor D1D - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
C:Accession: C55886
R:Demichyshyn, L.L.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, H.B.
J. Biol. Chem. 270, 4005-4012, 1995
A:Title: The dopamine D1D receptor. Cloning and characterization of three pharmacologic
A:Reference number: A55886; MUID:95181368
A:Accession: C55886
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-444 <DEM>
A:Cross-references: GB:L36879
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query Match 26.8%; Score 482; DB 2; Length 444;
Best Local Similarity 34.7%; Pred. No. 8.4e-33;
Matches 112; Conservative 57; Mismatches 114; Indels 40; Gaps 8;

```

```

Qy 21 VRASLTLNVLIIITLVNLIYVSIHFKOLHP-TNMLIHSMATVDFLGLCLMPSY 79
Db 11 LRRLGCLLGLAVLGLTAGLALVLRRLHRTKVTYMWVSLAISLCVAIILVMPK 70
Qy 80 MYRS-AEHCMYGEVFECKITHTSDIMLSSASIFHLSEISIDRYAVCDPLRYKAKMNLIV 138
Db 71 ATEVAGGFMLFGSRFCDFWVAFDIMCSTASILHLCITISIDRYWALASPRYERRMTR 130
Qy 139 ICVMITISVPAVAFGMIFLELNFGKAEIYYKHVHCRGCSVFFSKISGLVTMTSF 198
Db 131 ACAMIMAAWALISLISF--VPVOLHMHKAKD-----RRHSSSCDVSLNRTYATSSLSIS 184
Qy 199 YIPGSIIMLCVYRIYILIAKEQARLISDANOKIOLGEMKNG-----ISQSK 244
Db 185 YIPVAMITVYRIYILIAQRIIRIST-----LERAGGOMPASKEPASTLRSLRK 226
Qy 245 ERKAKVTGIYMGVFLICMCPFFICTVMDPLHY-----YIIPPLNDVLIHFGYLN 295
Db 237 ETKVLQTLISIMGVFCWMLPFLLNCLLPFCQPESDSNQSPCVQGTTFENVFWMGMAN 296
Qy 296 STENPMVYAFEPYFWRKALMKML 318
Db 297 SSVPVPIYAFNAD-FRRAFSNLL 318

```

```

RESULT 9
A55886
dopamine receptor D1A - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999

```

```

C:Accession: A55886
R:Demichyshyn, L.L.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, H.B.
J. Biol. Chem. 270, 4005-4012, 1995
A:Title: The dopamine D1D receptor. Cloning and characterization of three pharmacolog
A:Reference number: A55886; MUID:95181368
A:Accession: A55886
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-450 <DEM>
A:Cross-references: GB:L36877
A:Note: authors translated the codon MET for residue 427 as Ile, and ACC for residue
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query Match 26.8%; Score 482; DB 2; Length 450;
Best Local Similarity 34.6%; Pred. No. 8.6e-33;
Matches 113; Conservative 56; Mismatches 110; Indels 48; Gaps 8;

```

```

Qy 31 LIILITVGNLIVISISHFOLHP-TNMLIHSMATVDFLGLCLMPSYMSAEHCWY 89
Db 31 LILSLTGLNTLVCAVIRFRLHRSKVTFYISLAVSDLVAVLMPKAVSETAGFMP 90
Qy 90 FGEVFECKITHTSDIMLSSASIFHLSEISIDRYAVCDPLRYKAKMNLIVICVMIFISMSV 149
Db 91 FGS-FCNIVAVRDIMCSTASINLCVISYDRYWALASPRYERRMTRPKAFIMISVAMTL 149
Qy 150 PAVPAFGMIFLELNFGKAEIYYKHVHCRGCSVFFSKISGLVTMTSFYIPGS 203
Db 150 SVLISF--IPVOLHMHKAKATTSFLDNLASLOGISMDNCDSLNRMYAISSLSIFPIVA 207
Qy 204 IMCVYRIYILIAKEQARLIS-----DANOKIOLGEMKNGIS 241
Db 208 IMVYTRILYRIAQKQIRISALERAAYAKKQNTSGNRSSMDCCP-----ESNFKKS 262
Qy 242 OSKERRAVKTLGIYMGVFLICMCPFFICTVMDPLHY-----YIIPPLNDVLIH 291
Db 263 FKRETKVLKTLISIMGVFCWMLPFLLNCLLPFCQPESDSNQSPCVQGTTFENVFWMGMAN 322
Qy 292 GYLNSTENPMVYAFEPYFWRKALMKML 318
Db 323 GWANSSLNPIIYAFNAD-FRKAFTSL 348

```

```

RESULT 10
A51660
dopamine D1B receptor - African clawed frog (fragment)

```

```

C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51660
R:Sugamori, K.S.; Demichyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150
A:Accession: I51660
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-457 <SUG>
A:Cross-references: EMBL:007864; NID:9559761; PIDN:AAA50829.1; PID:9559762
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query Match 26.7%; Score 481; DB 2; Length 457;
Best Local Similarity 35.5%; Pred. No. 1.1e-32;
Matches 113; Conservative 54; Mismatches 121; Indels 30; Gaps 7;

```

```

Qy 27 SLNVLIIITVGNLIVISISHFOLHP-TNMLIHSMATVDFLGLCLMPSYMSVRSAB 85
Db 46 SLNVLIIITVGNLIVISISHFOLHP-TNMLIHSMATVDFLGLCLMPSYMSVRSAB 105
Qy 86 HCWYFGEVFECKITHTSDIMLSSASIFHLSEISIDRYAVCDPLRYKAKMNLIVICWIFI 145

```

Db 106 GHWFG-APCDIIVAFDIDMCSTASINLCVIVSDRYWAISSPRYERKMTQVALLMIST 164  
 QY 146 SWSVPAVFAFGMIFLELNFGKAEIYKHHVHRCGCGSVFESKISGVLTFMTSPYIPGS 204  
 Db 165 AMLSVLISF--IPVQLSMKSETEDHLNSHGNCDSLSNRYAIASSSLISFYIPVAI 222  
 QY 205 MLCVYRIYLIAREQARLISDANQKIQIGLEMKNG-----ISQSKERRAVK 250  
 Db 223 MIYTYRIYRIAQIQIRKISTLERAAHQAQSCRSNRVDSCSRHHQSTLRFISIKETVKL 282  
 QY 251 TLGIWGVFLICCPFFICTVMDPFLHY-----IIPPLINDVLIWFGYINSTFNP 300  
 Db 283 TLIISGVFVCCWLPFFILNCWPFCDRSPGHQAQGLPCVSETTFDLEWFGMANSSLP 342  
 QY 301 MYVAFYFPMFRKALKMML 318  
 Db 343 IITAFNAD-PRKVFSSLL 359

# RESULT 11

151659  
 dopamine D1A receptor - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 13-Aug-1999  
 C:Accession: I51659  
 R: Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994  
 A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.  
 A:Reference number: I51659; M01D:95024150  
 A:Accession: I51659  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-451 <SUG>  
 A:Cross-references: EMBL:U07863; NID:9559759; PIDN:AAA50828.1; PID:9559760  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: neurotransmitter receptor

Query Match 26.7%; Score 480; DB 2; Length 451;  
 Best Local Similarity 34.5%; Pred. No. 1.3e-32;

Matches 111; Conservative 56; Mismatches 117; Indels 38; Gaps 7;

QY 31 LIITLVGNLIVIVSISHFQKLTTP-TNMLIHSMTVDLGLVMPYSNVRSAEHCWY 89  
 Db 31 VLITSLTGLMTLCAAVIRFHLRSKVTNFEVSLAVSDLLVAVLWPMKVAEIAQWMP 90  
 QY 90 FGEVFCIKIHSTDMLSASIFHLFSIDRYAVCDPLRKAKANLILYCVIMFISMSV 149  
 Db 91 FG-TFCNIMWAFDIDMCSTASINLCVIVSDRYWAISSPRYERKMTQVALLMIST 149  
 QY 150 PAVFAFGMIFLELNFGKAEIY-----KHVHRCGCGSVFESKISGVLTFMTSPYIPGS 203  
 Db 150 SVLSF--IPVQLSMKSETEDHLNSHGNCDSLSNRYAIASSSLISFYIPVAI 207  
 QY 204 IMLCVYRIYLIAREQARLISDANQKIQIGLEMKNGISQ-----SKER 246  
 Db 208 IMIYTYRIYRIAQIQIRKISTLERAAHQAQSCRSNRVDSCSRHHQSTLRFISIKETVKL 267  
 QY 247 KAVTGLIGVFLICCPFFICTVMDPFLH-----YIIPPLINDVLIWFGYINSTFNP 296  
 Db 268 KVLTLGVIMVFCWLPFFILNCWPFCDRSPGHQAQGLPCVSETTFDLEWFGMANSSLP 327  
 QY 297 TFNPMVAFYFPMFRKALKMML 318  
 Db 328 SLNPIITAFNAD-PRKAFSSLL 348

# RESULT 12

S68423  
 serotonin receptor 1D alpha - rabbit  
 N:Alternate names: 5-hydroxytryptamine receptor 1D alpha (5-HT1Dalpha)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999

C:Accession: S68423  
 R:Harwood, G.; Lockyer, M.; Giles, H.; Fairweather, N.,  
 FEBS Lett. 377, 73-76, 1995  
 A:Title: Cloning and characterisation of the rabbit 5-HT(1D-alpha) and 5-HT(1D-beta)  
 A:Reference number: S68422; M01D:96130324  
 A:Accession: S68423  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HAR>  
 A:Cross-references: EMBL:Z50162; NID:91004281; PIDN:CAA90530.1; PID:91004282  
 C:Superfamily: octopamine receptor type I  
 C:Keywords: neurotransmitter receptor

Query Match 26.4%; Score 475; DB 2; Length 377;  
 Best Local Similarity 32.0%; Pred. No. 2.8e-32;

Matches 112; Conservative 62; Mismatches 120; Indels 56; Gaps 7;

QY 21 VRASLYSLMWLIITLVGNLIVIVSISHFQKLTTP-TNMLIHSMTVDLGLVMPYSM 80  
 Db 37 LKISLAVVLSIITVAVTAVLSTNFTVLTITLTKLTPANVYLGSLATYDLSILVMSI 96  
 QY 81 VRSAEHQWYGEVFCIKIHSTDMLSASIFHLFSIDRYAVCDPLRKAKANLILYCV 140  
 Db 97 AYTTHTWNGQVLCIDWVSSDICTTASILHLCVIALDRWALTDLKSKRTAGHAA 156  
 QY 141 VMPIFSVPAVFAFGMIFLELNFGKAEIYKHHVHRCGCGSVFESKIS-GVLTFMTSPY 199  
 Db 157 AMIYVVAISICISIPPLFMR-QAKAHEV-----SDCLVNTSQISITVITGCAFY 207  
 QY 200 IPGSIMLCVYRIYLIAREQ-----ARLISDA----- 226  
 Db 208 IPSVLLIVLGRYMAARNRILNPPSLYGRKFTAHILITGAGSSLSLSPSLGEGSHS 267  
 QY 227 -----NOKIQIGLEMKNGISQSKERRAVTGLIGVFLICCPFFICTVMDPFL 276  
 Db 268 AGSPLFENPVARIKLADSVLERKRISAREKATVTTGILGAFGCWLPFFVAVLPIIC 327  
 QY 277 H-YIIPPLINDVLIWFGYINSTFNPVAFYFPMFRKALKMML-FGKIE 323  
 Db 328 RDSQWMPFGLEDFFTWGLGYLNSLINPIITYVFNDFPDQAQORVIRHFKAF 377

# RESULT 13

A53279  
 serotonin receptor 1D - human  
 N:Alternate names: 5-hydroxytryptamine receptor 1D (5-HT1D); 5HT-1D alpha receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 05-Nov-1999  
 C:Accession: A53279; A44136  
 R:Hamblin, M.W.; Metcalf, M.A.  
 Mol. Pharmacol. 40, 143-148, 1991  
 A:Title: Primary structure and functional characterization of a human 5-HT-1D-type se  
 A:Reference number: A53279; M01D:91342595  
 A:Accession: A53279  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HAM>  
 A:Cross-references: GB:M81869; NID:9338023; PIDN:AAA60315.1; PID:9338024  
 C:Genetics:  
 A:Gene: GDB:HTRLD  
 A:Cross-references: GDB:132416; OMIM:182133  
 A:Map position: 1p36.3-1p34.3  
 A:Introns: #status absent  
 C:Superfamily: octopamine receptor type I  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran



Qy 308 PWFRRALKMMLFGKIFOKDSSRCKL 332  
| : : : : :  
Db 293 RDEFTGYQOLEFCRCRLANRNSHKTSL 317

Search completed: December 11, 2001, 16:09:21  
Job time: 98 sec

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OY 85 EHCWTFGEVCKIHTSTDMILSSASIFHLSTISIDRYAVCDPLRYKAKMNLIVICMIF 144
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 EHCWTFGEVCKIHTSTDMILSSASIFHLSTISIDRYAVCDPLRYKAKMNLIVICMIF 120
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 145 ISMSVPAAVAFGMIFELNFKGAEELIYKHVHRCGCCSVFESKISGLVFMSTFIPGSI 204
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 LCMVSPGAFAFAVSEAVADGIEG-YDILVACSSSCPWFNFNLMTGTTLFMAGFPGSN 179
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 205 MLCVYRILIKLEQARLISD--ANOKLOGLEMKNGISOSKREKAVNTGLIAGVGLLC 262
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 180 MGIYKIKRFAVRKHAHALNMLRENONNOY-----KKDKKAKTLIGIYGFLLC 229
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 263 WCPFFCTVMDPFLHYIIPPTLNDVLMFEGYLNSTFNPVYAEFYPMFRKALMFLGKI 322
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 WCPFFCTVMDPFLHYIIPPTLNDVLMFEGYLNSTFNPVYAEFYPMFRKALMFLGKI 289
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 323 F-----QKDS 327
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 290 FSSCFHNTILCMQKES 305
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

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RESULT 2
OY 09P14 PRELIMINARY; PRT; 343 AA.
AC 09P14;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE G PROTEIN-COUPLED RECEPTOR 57.
GN GPR37.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT "Cloning and characterization of additional members of the G protein-
RT coupled receptor family."
RL Biochim. Biophys. Acta 1490:311-323(2000).
DR EMBL; AF112461; AAF27279.1; -.
DR InterPro: IPR002106; G_PROTEIN_Ligase_II.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00339; AA-TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KV Receptor.
SQ SEQUENCE 343 AA; 39065 MW; DC513D15ABBC026F CRC64;
```

Query Match 45.2%; Score 813.5; DB 4; Length 343;  
Best Local Similarity 46.0%; Pred. No. 2.9e-58;  
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

```
OY 4 CHNIIN-----ISCVKNN-----WSNDYRASLSLMVLIITLVGNLIVISISH 49
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 13 CKEFVKILSSHQPLFSCDGNVFGYDMSHDY-----PLFGNLIIVISISH 58
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 50 EQQLHTPTMNLHSMATVDFLLGLCLVMPYSAMRSACHWTFGEVCKIHTSTDMILSSAS 109
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 EQQLHTPTMNLHSMATVDFLLGLCLVMPYSAMRSACHWTFGEVCKIHTSTDMILSSAS 118
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 110 IPHLSPISTDRYAVCDPLRYKAKMNLIVICWIFISMSVPAVFAFGMFLDNFGAE 169
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 119 IPHLSPISTDRYAVCDPLRYKAKMNLIVICWIFISMSVPAVFAFGMFLDNFGAE 178
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 170 IYKVVHCHGCGSVFESKISGLVFMSTFIPGSI-MLCVYRILIKLEQARLISDANOK 229
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
DB 179 -YKILVACFNCALETNKGWILLFTTCFPPSGINWGIYKIFIVSKOHARIYSHPEN 237
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 230 LOIGLEMKNGISOSKREKAVNTGLIAGVGLLCWCPFFCTVMDPFLHYIIPPTLNDVLI 289
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 238 TKGA--YKHLKSKDKKAKKTLIGIYGVFLACWLCFLVNLIDPILDIYSTPILIIDLY 295
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 290 WFCYLNSTFNPVYAEFYPMFRKALMFLGKIFQDSSRCKLFLF 335
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 296 WLFYFNSTCNPLIHGFNFPMFOKAFYIVSGKLFSSHSRTANLPFE 341
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

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RESULT 3
OY 014804 PRELIMINARY; PRT; 337 AA.
AC 014804;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE PUTATIVE NEUROTRANSMITTER RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98125534; PubMed=9464258;
RA Zeng Z., Fan P., Rand E., Kyaw H., Su K., Madike V., Carter K.C.,
RA Li Y.;
RT "Cloning of a putative human neurotransmitter receptor expressed in
RT skeletal muscle and brain."
RL Biochem. Biophys. Res. Commun. 242:575-578(1998).
DR EMBL; AF021818; AAC39581.1; -.
DR InterPro: IPR000832; GPCR_Rhodopsn.
DR InterPro: IPR001917; Aminotransf_2.
DR Pfam; PF00001; 7tm_1; 2.
DR PROSITE; PS00599; AA-TRANSFER_CLASS_2; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KV Receptor.
SQ SEQUENCE 337 AA; 38300 MW; 32134652B85CB35A CRC64;
```

Query Match 37.6%; Score 677.5; DB 4; Length 337;  
Best Local Similarity 39.0%; Pred. No. 2.9e-47;  
Matches 130; Conservative 67; Mismatches 125; Indels 11; Gaps 4;

```
OY 3 FCHNIINISCVKNNMSNDYRASLSLMVLIITLVGNLIVISISHFQQLHTPTMNLH 62
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 16 FCYQ-VNGSOPRVHTLGIQLVLYIFCAAGMLIIVGNVAVAFYKALHTPTMNLH 74
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 63 SMATVDFLLGLCLVMPYSAMRSACHWTFGEVCKIHTSTDMILSSASIFHLSTISIDRY 122
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 75 SLALDMFGLVPLPLSTIRSVESCWFFGDFLCRLHTYDLECLTISIFHLCTISIDRIG 134
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 123 AVCDPLRYKAKMNLIVICWIFISMSVPAVFAFGMFLDNFGAEIYKHVHRCGCCS 182
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 135 ALCDPLRYKAKMNLIVICWIFISMSVPAVFAFGMFLDNFGAEIYKHVHRCGCCS 193
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 183 VPFKISGLVFMSTFIPGSI-MLCVYRILIKLEQARLISDANOKLOIGLEMKNGIS 242
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 194 LILNKFWMGLNF-PLFVFCILMISLYVKIFVATRQAOQITLSSSL-----AGAA 244
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 243 SKREKAVNTGLIAGVGLLCWCPFFCTVMDPFLHYIIPPTLNDVLIIMFEGYLNSTFNPV 302
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 245 KHKRAKAKTLIGIYGVFLACWLCFLVNLIDPILDIYSTPILIIDLY 304
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 303 YAEFYPMFRKALMFLGKIFQDSSRCKLFLF 335
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 305 YVFSYQFRKALMFLGKIFQDSSRCKLFLF 337
    1:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 4

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Q9YHY4 PRELIMINARY: PRT: 352 AA.
ID Q9YHY4
AC Q9YHY4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE ODORANT RECEPTOR LOR3.
OS Lampetra fluvialilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=OLFATORY;
RA Bernhard A., Dryer L.;
RT "A novel family of ancient vertebrate odorant receptors.";
RL J. Neurobiol. 0:0-0(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF069546; AAC82381.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR KEGG: G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40276 MW; 6366743DCFFA9FAE CRC64;

Query Match 32.2%; Score 580.5; DB 13; Length 352;
Best Local Similarity 36.6%; Pred. No. 2,1e-39;
Matches 121; Conservative 69; Mismatches 132; Indels 9; Gaps 5;

QY 9 NISCVKNNMSNDVRSASYSLSMLVLIITLVGNLIVYISISHPKOLHPTNMLISMATVD 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 18 NEKTLSELTPQPVRLVLIWFTIIITTVGNILITVSIKFRQLQRTNVLALSALAD 77
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 FLIGCLVMPYSVRSABHCWYFGEVFCIKHTSTDIMLSASIFHLFSIDRYAVCDPL 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 FLVCLIMPFVSMRTAVASCWFGOLMCRHITWLDYFTTCSIFNLACISIDRYAVISDPL 137
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 RYKAKMNLIVICWIFISMSVPVAFAGMIF-LELNFGAEIYIKKHVHGCGGCVFEFSK 187
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 RYDRAVYRIALVMLTTCWG--NIIPGVSYMLKINGISVVAAK-SCPDNCSVFEMNV 194
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 ISGVLTFTSFYIPGSIIMLCVYRIRYILAKEOARLISDANKLOIG----LEMKNGISQS 243
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 195 PFGIANSKGAIVLPLFTMAIYSRITYVARNQAKRISLSIGQVRASNSADLTMSKMMAM 254
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 K-EKRAVKTIGVGVFLICWCPFFICTVMDPFLHYIIPTLNDVLIVFGYLNSTFNPV 302
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 KRDNNAFTGLMIMVLTFLVPLFIVAVATEPVIGRYMDSTVMDVANNFTFNSMNPIL 314
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 303 YAFEPYWRKALKMMLFGKITFOKDSRCKLF 333
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 315 FASFNNSFRSAFYILMSGIILRGYRGTDLF 345
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
ID Q9YHY8 PRELIMINARY: PRT: 328 AA.
AC Q9YHY8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE NEURONTRANSMITTER RECEPTOR.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN
RP

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RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Reboul J., Gardiner K., Uze G., Lutfalla G.;
RT "Class II cytokine receptor gene cluster is fixed in amniotes.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF083221; AAC96117.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR KEGG: G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 328 AA; 36526 MW; 687757B373198CC CRC64;

Query Match 30.3%; Score 545.5; DB 13; Length 328;
Best Local Similarity 35.4%; Pred. No. 1.3e-36;
Matches 119; Conservative 65; Mismatches 127; Indels 25; Gaps 5;

QY 4 CHNIIISCVKNNMSNDVRSASYSLSMLVLIITLVGNLIVYISISHPKOLHPTNMLIHS 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 CFANLNSCKRLNQTFFSTAVFSSLSASVLTITVLNLVLIISHPKOLHPTNLTLLS 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 MATVDFLLGCLVMPYSVRSABHCWYFGEVFCIKHTSTDIMLSASIFHLFSIDRYA 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 LAVSDLVGLVLMPIEGRLVYEMCMWLGSLMCALTPVYSCVLSASVGNMVLISIDRYLA 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 VCDPLRYKAKMNLIVICWIFISMSVPVAFAGMIFLELNFGAEIYIKKHVHGCGGCV 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 ICDPLTYTKVTLVTRAKIATLCWACSLLYNGSILMGLHQP-----RINSGECV 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 FFSKISGVLTFTSFYIPGSIIMLCVYRIRYILAKEOARLISDANKLOIGLEMKNGISO- 242
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VISHSGVDEFTFVLCVAVVVMVFIATAVQNMVIRQNVALLV-----NAASRV 238
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 -SKERRAVKTIGVGVFLICWCPFFICTVMDPFLHYIIPTLND-----VLIVFGYLN 296
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 TKSEKKAARTGIIVTFLCECPYYPALAG-----GDTSNMISYFAVLSWIMTINS 291
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 TFPNPAVYAFEPYWRKALKMMLFGKITFOKDSRCKL 332
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 CVNPLIALFYPWFRRSIKLIVTEKILRLYSNDIKL 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
ID Q9H199 PRELIMINARY: PRT: 359 AA.
AC Q9H199;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE 5-HYDROXYTRYPTAMINE4 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN (HIPPOCAMPUS);
RA Villaro M.T., Domenech T., Palacios J.M., Mengod G.;
RT "Cloning and characterization of multiple human 5-HT4 receptor variants including a novel variant that lacks the alternatively spliced C-terminal exon.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AJ278982; CAC22251.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.

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DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1: 1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2: 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane  
SQ SEQUENCE 359 AA; 40797 MW; C6B033F18178AF3 CRC64;

OY	230	LQIGLEMKNGISG-----KERKAVTLGIWGFELICMCPEFTICTVMDPFL	276
Db	235	LQVIAQQQQQQQAEPNIRIKWTAMRKHEHSAKTLSGITGYLLSMPLFRTVVLFFP--	292
OY	277	HYIIPPLNDLVLMFGYLNSTFNPNVAFFYFWFRKALKMMLFGKIIFOKDSSR	329
Db	293	NFOSSAAVRITTTWIGYTSSAINPVLYATLNPFRSFAFVAIVSCVLSSTRAR	345
RESULT	9		
ID	042315	PRELIMINARY;	PRT; 446 AA.
AC	042315;		
DT	01-JAN-1998	(TREMBLrel. 05, created)	
DT	01-JAN-1998	(TREMBLrel. 05, last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, last annotation update)	
DE	DLA3 DOPAMINE RECEPTOR.		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Acyinopterygii; Neopterygii; Telostei; Euteleostei; Ostariophysi;		
CC	Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.		
OX	MCL_TaxID=7962;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=RETINA;		
RA	Hirano J., Archer S.N., Djamgoz M.B.A.;		
RL	Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARTY).		
CC	-1- SIMILARTY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL; Y146Z6; CAA74970.1; -		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRRHODOPS.		
DR	PROSITE; PS00237; G_PROTEIN_RECPT_F1.1; 1.		
KM	PROSITE; PS50262; G_PROTEIN_RECPT_F1.2; 1.		
SW	G-protein coupled receptor; Glycoprotein; Transmembrane.		
SQ	SEQUENCE 446 AA; 49600 MW; 417834A303627D20 CRC64;		
Query Match	27.9%; Score 503; DB 13; Length 446;		
Best Local Similarity	34.7%; Pred. No. 5e-33;		
Matches 118; Conservative 68; Mismatches 120; Indels 34; Gaps 10;			
OY	7	IINISCVKNNSNDVRASLYSLAVLIILTTLVGNLIYVISHSFKQLHTP-TNNLIHSM A	65
Db	8	VLDSSVSQRNSSKRVLTCGF--LSILLMTTLLIGNLVCAAWTKFRHLRSKVTFEYISA	65
OY	66	TVDPELLGLVMYSNVBSAEHCWVGCEVPCKINHSTDIMLSASFHLFSITDDRYAAC	125
Db	66	ISDLLVALVLLWMKATELVGEFMPFG-AFCDWVAFEDICSTASTLNLCLVISVDRIWALS	124
OY	126	DLARKAKMNILVICVMIFISWSVPAVPAFGMIFELNFLKGAEELYKKHHCRGG----	180
Db	125	SPFRERKMTPRVARTIMSVAMTLLISLF--IPQALMHKKQADSYTELNTGYELPRD	182
OY	181	-CSVFESKISGVLTMTSPFYTGSIIMLCVYYNYLIAEQALL-----SDANOQIQ	231
Db	183	NCDSSLNRFYALSSLSISFYIPVALMITYTRTYIAKQIRRIASALERAAESANNRHSS	242
OY	232	IG----LEMKNGISG--KERKAVTLGIWGFELICMCPEFTICTVMDPFL-----Y	278
Db	243	MGNNSMESSESFKKSFRKETVLTLSIVKMGVFCWCMLPFVLMCMVFCFPNNESSDF	302
OY	279	IIPPLNDLVLMFGYLNSTFNPNVAFFYFWFRKALKMML	318
Db	303	CISTTFDVVFVWFGWANSINLPIIYA FNAD-PRKAFTSL	341
RESULT	10		
ID	098842	PRELIMINARY;	PRT; 445 AA.
AC	098842;		
DT	01-FEB-1997	(TREMBLrel. 02, created)	

DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE DOPAMINE D1A2 RECEPTOR.  
GN D1A2.  
OS Anguilla anguilla (European freshwater eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguillidae; Anguilla.  
OX NCBI\_TaxId=7936;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97160583; PubMed=9006917;  
RA Cardinaud B., Coudouet S., Vincent J.D., Vernier P.;  
RT "Early emergence of three dopamine D1 receptor subtypes in  
RT vertebrates. Molecular phylogenetic, pharmacological, and functional  
RT criteria defining D1A, D1B, and D1C receptors in European eel *Anguilla  
RT anguilla*."  
RT J. Biol. Chem. 272:2778-2787 (1997).  
RC 1-1 SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC EMBL: U62919; AAC60069.1; -  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR InterPro: IPR000209; Peptidase\_S8.  
DR pfam: PF00001; 7tm1.1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPSN.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE: PS00136; SUBTILASE\_ASP; UNKNOWN.1.  
KW G-Protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 445 AA; 49310 MW; B433AD81C1C1439 CRC64;

	Query Match	27.7%	Score 498.5:	DB 13:	Length 445;	
	Best Local Similarity	34.1%	Pred. No. 1.2e-32:			
	Matches 118:	Conservative 66:	Mismatches 123:	Indels 39:	Gaps	9:
Oy	8 INISCVKNNMNDPRAASYLSL----	MVLIIITLVGNLIYVISISHFQKLHTP--TNMLIH 62				
Dd	3 LNFSTVLDGSLSEIDSSRVRLTGLCESSLIYSTLLGNLTVAACAAVKPRH;ASKVTNFEVI 62					
Oy	63 SMAIVDFLLGLWMPYSWNVRSAEHWCYTGEVFCKTHSTDIMLSASAFPHLSFISIDRY 122					
Dd	63 SLAVSDLLVALILVMFKAVTEVAGFWPGES--FCNTIWAFFDIMCSYASALINCILISVDRY 121					
Oy	123 AVCPDLRKAKNNILIYOVMTFISNSVAPFAFGMFIPLEINKGADEI--YKKHVHCRC-- 179					
Dd	122 AHSFERERKTKPVARVAMSVAAITLSLSE--IPVLNMHKKQTTSYFDHNGSYDCL 179					
Oy	180 ---GCSTVFPSKISGVLTFTMSFYIGSITMLCYRIRYLIAKEOARLISDAOKIOGLEM 236					
Dd	180 LLDNCDDSLNRKYAIASSLSISFYIPVALIVITYTRITRIAQOKLRISALEBMAASAANKR 239					
Oy	237 KNGISO-----KERKAVKTGLVGVEFLICWCPEPFICYMDPLHYIIP- 281					
Dd	240 HNSMNSSSVETESSFKMSKFRETFLVTLTSIVMCVFCOCWPIFLINCMWPFCBOAHPN 299					
Oy	282 -----PTINDVLIMEGYLNSFNFMNVYAFAFPWRPKALKKML 318					
Dd	300 GSADEPCVYSTTENVFWMFGMANSSLPLTIYNAD--FRKASFILL 344					
	RESULT 11					
ID	042316					
AC	042316 PRELIMINARY: PRT: 437 AA.					
DT	01-JAN-1998 (TREMBLrel. 05, Created)					
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)					
DS	D1A4 DOPAMINE RECEPTOR.					
OS	Cyprius carpio (Common carp).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Ostariophysi;					
OC	Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.					



DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPS\_N.  
DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 397 AA; 44793 MW; BB4719084F4BD59 CRC64;

Query Match 27.1%; Score 488.5; DB 11; Length 397;  
Best Local Similarity 34.8%; Pred. No. 6.6e-32;  
Matches 114; Conservative 56; Mismatches 111; Indels 47; Gaps 7;

QY 30 VLIITLTVL-----GNLIVISIFHKQLHTPTNMLIHSMTVDLGLCYMPSMVRSA 84  
DB 21 ISVLTLLIFITVAGNVVCLAVSLNRLRLSLTNCFIYSLATDLDLGLVWPEFAITQL 80  
QY 85 EHCWTFGEVFCIKHTSTDIMLSSASIFHLSTIDRYAVCDPLRYKAKNMILVICWIF 144  
DB 81 SFKSFQGVFCNIYTSIDVMTCTASILNLFMISIDRYCAVTDPLRYPVLPVRAVLSLV 140  
QY 145 ISMSPAVFAFGMIFELNFKGAEIYYKHVCRG-----CSVPEFSKISGVLFMTSFY 199  
DB 141 FIWVISTLSLSTLHGLNNSRNG-----TRGNDTFCKCKVQVNEVYGLVGMVTFY 191  
QY 200 IPGSIMLCVYRIYLIAKEQARLISDANQKIQIGLEMKNGISQSK-----ERKAVKTGI 254  
DB 192 LPLIMCVTYRIRFKIAREQAKRI-----NHISMKAAITIREKAVITLAA 237  
QY 255 VMGFVFLICWCFEICTV-----DFPLHYIIPPTLNDVLINEGYLSTFNPMVAFEPFW 309  
DB 238 VMGFVFCVCFEICTVAFYVYRGLRGDVAENEV-----EGIVLMGVANSALNPITVATLNRD 293  
QY 310 FRKALKMMLFGKIFOKDSSRCKLFELS 337  
DB 294 FRMAVQQLFCKLASHNSHKTSLRLNS 321

## RESULT 14

Q98841 PRELIMINARY; PRT: 445 AA.  
AC Q98841;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE DOPAMINE D1A1 RECEPTOR.  
GN D1A1  
OS Anguilla anguilla (European freshwater eel).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguillidae; Anguilla.  
OX NCBI\_TaxID=7936;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-97160583; PubMed-9006917;  
RA Cardinaud B., Coudouel S., Vincent J.D., Vernier P.;  
RT "Early emergence of three dopamine D1 receptor subtypes in  
vertebrates. Molecular phylogenetic, pharmacological, and functional  
criteria defining D1A, D1B, and D1C receptors in European eel Anguilla  
anguilla.";  
RL J. Biol. Chem. 272:2778-2787(1997).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL: U62918; AAC60067.1; -;  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPS\_N.  
DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 445 AA; 49442 MW; 2A26D945DE39ACDD CRC64;

Query Match 27.1%; Score 488.5; DB 13; Length 445;  
Best Local Similarity 35.0%; Pred. No. 7.4e-32;  
Matches 111; Conservative 61; Mismatches 112; Indels 33; Gaps 8;

QY 31 LIITLTVGNLIVIVISIFHKQLHPT-TNMLIHSMTVDLGLCYMPSMVRSAEHCWY 89  
DB 30 LIITLTVGNLIVCAVTRFRLNRKVTNFEVYSLSLSDLLVAIILVPMKATTEIVGFWP 89  
QY 90 FGEVFCIKHTSTDIMLSSASIFHLSTIDRYAVCDPLRYKAKNMILVICWIFISMSV 149  
DB 90 FGS-FCNVWVAFEDINCSTASILNLCVISDRWMAISSPFYRKMTPVAFMISVAMTL 148  
QY 150 PAVFAFGMIFELNFKGAEIYYKHVCR-----GGCVPEFSKISGVLFMTSFYIPG 202  
DB 149 SVLISF--IPVQLMHNKKAQAGFPELNGTFREPPRPDCCSLNRTVYAISSLSLFIYV 206  
QY 203 SIMLCVYRIYLIAKEQARLIS-----DAQKIQIGLEMKNGISQSK-----ERKAVK 250  
DB 207 AIMIVTYRIRYIAQKQIRISALERAASAKNRHSSMGNSIESSEFSKMSFKRETQVAK 266  
QY 251 TLGIWVGFLLICWCFEICTVMDPLHY-----IIPPTLNDVLINEGYLSTFNPM 301  
DB 267 TLSTVINGVFCVCMLEFLLINCWVPCEQAPQAGADLPVCSSTTFDFVFWGANSLSLNDI 326  
QY 302 VYAFYVPMFRKALKMML 318  
DB 327 IYAFNAD-FRKAFSTLL 342

## RESULT 15

Q98844 PRELIMINARY; PRT: 448 AA.  
AC Q98844;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE DOPAMINE D1C RECEPTOR.  
GN D1C  
OS Anguilla anguilla (European freshwater eel).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguillidae; Anguilla.  
OX NCBI\_TaxID=7936;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-97160583; PubMed-9006917;  
RA Cardinaud B., Coudouel S., Vincent J.D., Vernier P.;  
RT "Early emergence of three dopamine D1 receptor subtypes in  
vertebrates. Molecular phylogenetic, pharmacological, and functional  
criteria defining D1A, D1B, and D1C receptors in European eel Anguilla  
anguilla.";  
RL J. Biol. Chem. 272:2778-2787(1997).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL: U62921; AAC60068.1; -;  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPS\_N.  
DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 448 AA; 50084 MW; 0ABC0296650B29F3 CRC64;

Query Match 26.7%; Score 481; DB 13; Length 448;  
Best Local Similarity 35.1%; Pred. No. 3e-31;  
Matches 113; Conservative 61; Mismatches 116; Indels 32; Gaps 10;

QY 21 VRASYSLSLWLIITLTVGNLIVIVISIFHKQLHPT-TNMLIHSMTVDLGLCYMPS 79  
DB 24 IVALGCVLFLLIVSTLGNLTVCYCAVYKFRHLRSKVTNFEVYSLSLSDLPFAVAVLMPK 83  
QY 80 MVRSAEHCWTFGEVFCIKHTSTDIMLSSASIFHLSTIDRYAVCDPLRYKAKNMILVI 139

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Db      84 AVSEVAGYWLFGK-FCETWIAFDIMCSTASINLCIISVDRYWAIASPFYERKMTORVA 142
Qy      140 CYMIFISMSVPRAVEAFGMIFLEINFKAGEIY-----YKHVHCRCGCSVFFSKISGVLP 194
Db      143 FIMIGVAMTSLIILISF--IPVOLMWHKAEEDYADDNSSNHTF--DCNMSLNSYVAISSS 197
Qy      195 MTSFYIPGSIIMLCVYYRIYLIKEQARLISDANOKLO-----IGLEMKNGISQS--K 244
Db      198 LISFYIPVYIMIGTYRIRIRIAOTOIRISSLERAVEQASHOHPSDCANENSLKTTFFK 257
Qy      245 ERKAVKTLIGIVNGVELICWCPPEICTVMDPLHY-----IIPPTLNDVLIIMFGYLS 296
Db      258 ETKVLTLSIIMGVFECWLPFEVLNCAWVPFCDIGEIDPLCYSDSTFN-IFWFGMANS 316
Qy      297 TFNPMYYAFEPYPERKALKML 318
Db      317 SLNPVIYAFNAD-FRKAFFSTIL 337
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Job time: 164 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 11, 2001, 16:07:43  
(Search time 24.1 seconds  
(without alignments)  
1038.870 million cell updates/sec)

Title: US-09-633-145-2

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Total number of hits satisfying chosen parameters: 522463

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Minimum DB seq length: 0
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Post-processing:  Minimum Match 0%
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**Pred. NO.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1801	100.0	339	22	AAG80973	Human ngPCR56 #3.
2	1801	100.0	339	22	AAB49232	Human SNORF33 rece
3	1520	84.4	296	22	AAG80972	Human ngPCR56 #2.
4	1403	77.9	332	22	AAB49231	Rat SNORF33 rece
5	1351	75.0	332	22	AAB49234	Mouse SNORF33 rece
6	1207	67.0	338	22	AAG80960	Human ngPCR56 #1.
7	998	55.4	191	22	AAB49230	Human SNORF33 rece
8	820	45.5	319	22	AAG72332	Human OR-like poly
9	817	45.4	306	18	AAW35631	Human G protein co
10	814.5	45.2	295	18	AAW72601	Human OR-like poly
11	813.5	45.2	343	19	AAW53907	Human HNHCl32 (G-P

12	782	43.4	338	21	AA8187655
13	743	41.3	348	21	AA8187656
14	715	39.7	345	22	AA8089070
15	677.5	37.6	337	18	AA809110
16	677.5	37.6	337	20	AA813736
17	614.5	34.1	225	18	AA8358333
18	614.5	34.1	225	18	AA8154222
19	558.5	31.0	312	22	AA8729668
20	534	29.7	360	20	AA1145220
21	534	29.7	380	20	AA1454521
22	534	29.7	426	22	AA8595727
23	526	29.2	387	15	AA8570229
24	524	29.1	402	22	AA8595733
25	522	29.0	406	15	AA8570330
26	521	28.9	264	22	AA8726111
27	509	28.3	388	15	AA8570051
28	485.5	27.0	241	22	AA8680951
29	478.5	26.6	376	12	AA8151373
30	474	26.3	377	20	AA8283033
31	474	26.3	377	22	AA8471855
32	472.5	26.2	359	20	AA8008888
33	472.5	26.2	359	21	AA8571172
34	467.5	26.0	374	13	AA8550494
35	461.5	25.6	348	17	AA8005551
36	461.5	25.6	348	18	AA8317122
37	458	25.4	446	12	AA8154688
38	458	25.4	446	14	AA8383664
39	455.5	25.3	477	13	AA8210812
40	454.5	25.2	477	16	AA8193182
41	454.5	25.2	477	18	AA8408020
42	453.5	25.2	446	12	AA8154598
43	453.5	25.2	757	14	AA8304977
44	452	25.1	418	14	AA8305050
45	450	25.0	390	10	AA8905501

## ALIGNMENTS

RESULT	1
AAAG80973	
ID	AAAG80973 standard; Protein; 339 AA.
XX	
AC	
XX	
XX	AAAG80973;
DT	28-AUG-2001 (first entry)
XX	
DE	
XX	Human ngPCR56 #3.
KW	G protein-coupled receptor; ngPCR;
KW	signal transduction; schizophrenia;
KW	rheumatoid arthritis; CNS disorder;
KW	cardiovascular disease; proliferat-
KW	neurological disorder; neuronal dis-
KW	attention deficit hyperactivity dis-
KW	Parkinson's disease; migraine; sena-
KW	rheumatoid arthritis; autoimmune di-
XX	neuroprotective.
XX	
OS	Homo sapiens.
XX	
PN	WO200136473-A2.
XX	
XX	
PD	25-MAY-2001.
XX	
PF	16-NOV-2000; 2000MO-US31581.
XX	
PR	16-NOV-1999; 99US-0165638.
PR	17-NOV-1999; 99US-0166071.
PR	19-NOV-1999; 99US-0166678.
PR	28-DEC-1999; 99US-0173396.
PR	22-FEB-2000; 2000US-0184129.
PR	28-FEB-2000; 2000US-0185421.

Amino acid sequence  
Amino acid sequence  
Human nGPRCRA0 #2.  
Human amine receptor  
Plasmid pUD-BL5 hu  
G protein coupled re  
human olfactory rec  
human serotonin re  
human serotonin re  
Human 5-HT4(1) rec  
Human 5-HT4 recep  
Rat 5-HT4 receptor  
Pdg 5-HT4(h) recep  
Rat 5-HT4 receptor  
Human OR-like poly  
Human serotonin re  
Human nGPRK3. Ho  
Human serotonin 1D  
Serotonin receptor  
5-hydroxytryptam  
human histamine H2  
sequence of HuH2R.  
5HT1 (serotonin) r  
human histamine H2  
protein sequence o  
Human dopamine D1  
Human dopamine D1  
Dopamine D1 recept  
Dopamine receptor  
Human D5 dopamine  
Rat dopamine D1 re  
N-terminal of LH r  
Hamster Delta-2 ad

PR 28-FEB-2000; 2000US-0185554.  
PR 02-MAR-2000; 2000US-0186330.  
PR 03-MAR-2000; 2000US-0186811.  
PR 09-MAR-2000; 2000US-0188114.  
PR 17-MAR-2000; 2000US-0190310.  
PR 21-MAR-2000; 2000US-0190800.  
PR 20-APR-2000; 2000US-0198568.  
PR 02-MAY-2000; 2000US-0201190.  
PR 08-MAY-2000; 2000US-0203111.  
PR 25-MAY-2000; 2000US-0207094.  
XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI Vogel I G, Wood LS, Parodi LA, Riebsch RR, Lind P, Slightom J;  
PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;  
XX  
DR WPI: 2001-389826/41.  
DR N-PSDB; AAH51013.  
XX  
XX New G protein-coupled receptor (nGPCR-x) and its encoding  
PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -  
XX  
XX Claim 37; Page 92; 261pp; English.

CC The present invention relates to novel G protein-coupled receptors  
CC (GPCRs; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,  
CC 28, 31-39, 40, 41, 53-60) and their coding sequences. The present  
CC sequence is one such G protein-coupled receptor. GPCRs are also known as  
CC seven transmembrane receptors and function in signal transduction. The  
CC nGPCR coding sequences are useful for screening a human to diagnose a  
CC disorder affecting the brain or a genetic predisposition, specifically  
CC schizophrenia. nGPCRx are useful for identifying compounds useful for  
CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a  
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal  
CC failure, rheumatoid arthritis, CNS disorders, infectious such as HIV-1,  
CC metabolic and cardiovascular diseases, proliferative disorders and  
CC hormonal disorders. Modulators of nGPCRx activity have the utility for  
CC treating neurological disorders, including schizophrenia, ADHD/ADD  
CC (attention deficit-hyperactivity disorder)/attention deficit disorder),  
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,  
CC migraine and senile dementia. Additional disorders include inflammatory  
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune  
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory  
CC diseases e.g. inflammatory bowel disease.

Query Match	100.0%	Score 1801,	DB 22,	Length 339,
Best Local Similarity	100.0%	Pred. No. 2,5e-200,		
Matches 338; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	MPFCHNIINTISCVNNNSNDVRAJLSJMWLIITFTLVGNLIYVSI:SHKROLHTPNML	60
Qy	2	mpfchnlintiscvnnnsndvrajsylmwliitftlvgnliyvs:shkqlhtpcnwl	61
Qy	61	IHSATVDFLLGCLVMPYSWVRSAEHCWYFGEVFCIKHTSTDIMLSASIFHLSFISDR	120
Db	62	lshmatvdflllgclvmpysmwrsaeohcwfygevfcklhtstdlmsaasifhsfisdtr	121
Qy	121	YAAACDLPKAKANNILVICWFIISMSVAVAFAGFIPIELNFKGAEIYKRVHVRGG	180
Db	122	yaaacdpklyrkaknnlilvicwfilismsvavafagfipielnfkgaeelykrvhvrvg	181
Qy	181	CSVFESKISGVLFPMTSFYIPGSIIMLCVYRIYLIKAQEARLISDAQOKIQIGHEMKNGI	240
Db	182	csvfeskisgvlftmetsfyipgsimlcvyryyliakeqearlisdanqkqidglemknjl	241
Qy	241	SOSKEKRAYTIGVACVVELICMCPPICTVMPDBFLHYITPPLINDVLMFGGLNSTFNP	300
Db	242	soskerkayvtligvacvvelicmcpipictvmpdbflhyitpplindvlmfvglnstfnp	301
Qy	301	MYVAFEPMPERKALKMMLFGKIFOKDSSRCKLELIS	338

[illegible]

AK 712367

DT 14-MAR-2001 (first entry)  
XX  
XX  
DE Human SNORF33 receptor protein.  
KW SNORF33; inflammation; arthritis; neurological disorder; infection;  
KW bone disease; respiratory disorder; asthma; cancer; cardiovascular.  
OS Homo sapiens.  
XX WC200073449-A1.  
XX  
XX  
PD 07-DEC-2000.  
XX  
XX 26-MAY-2000; 2000WO-US14654.  
XX  
XX 28-MAY-1999; 99US-0322257.  
XX 06-OCT-1999; 99US-0413433.  
XX  
XX (SYNA-) SYNAPTIC PHARM CORP.  
XX  
PI Borowsky BE, Ogozalek KL, Jones KA;  
XX  
XX WPI; 2001-025252/03.  
DR  
XX  
XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33  
PT receptor which is useful for designing drugs for treating conditions  
PT such as a chronic and acute inflammation, arthritis, neurological  
PT disorders and microbial infections -  
XX  
XX  
XX  
PS Claim 9; Fig 6; 227pp; English.  
XX  
XX  
XX The present invention relates to a mammalian SNORF33 receptor.  
CC SNORF33 antagonists and agonists are used to treat  
CC abnormalities brought about by increased or decreased activity of the  
CC mammalian SNORF33 receptor. The receptor is useful as a tool for  
CC designing drugs for treating conditions such as a chronic and  
CC acute inflammation, arthritis, neurological disorders, microbial  
CC infections, bone diseases, respiratory disorders such as asthma,  
CC cancers, cardiovascular disorders.  
XX  
XX Sequence 339 AA.

Query Match	100.0%;	Score 1801;	DB 22;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 2.5e-200;		
Matches 338; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MPENNIINISGVKNNKNSNDXRASLVSAMLLILTLTUGNLVIVYSISHPQOLHTPTNNML	60
	2	mpcchlllnhiscvknnsndvraa ysalm lllltcllygnlllvivsishfnglhtptw	61
Db			
QY	61	IHSMATVDFELLGCTLVMPESWMSAEHCWYGEVFCFKIRHSTDIMLSASIFHLSFISDR	120
QY	62	hsmatvdflllgclmppswnvraeehcwygefc cklnhstcdim sca shfshstf sdr	121
Db			
QY	121	YVAVCDPLRYAKKNNILVLCWMIETISWSNPAVFAFGMIELDLNFKGAEIYYKHHVRCG	180
QY	122	yyavcdplryaknm lvicwm etiswsn pavafagm el elnfkgaee yykhvrcrg	181
Db			
QY	181	GVFFSKTSISGVLTWTSTFYIPGSIIMLCVYRIRYLAKEDARLISANOKLOIGEMKNGI	240
	182	gvfffsk s sgy ltm es fy pgs im cvy r yl ak ega arl s an ok lo ig em kng	241

QY	241	SOSKERRAKVLTGLVAGVFLICWCPEFTICVMDPEFLHITIPPLINDVLIWEGILNSTEND	300
Db	242	sqsketkavkclglvmgvfljicwcpffictcmdbflhyilprclndvliwfgylnstfnp	301
OY	301	MVAFEPWPFRRALKMMLFGKIFPKDSSRCKLFELESS	338
Db	302	mvaftfpwftkalkmmlfgklfqkdsrrcklfele ss	339
RESULT 3			
ID	AA680972	standard; Protein: 296 AA.	
AC	AA680972:		
XX			
DT	28-AUG-2001	(first entry)	
XX			
DE	Human ngPCR56 #2.		
XX			
KW	G protein-coupled receptor; ngPCR; seven transmembrane receptor;		
KW	signal transduction; schizophrenia; thyroid disorder; renal failure;		
KW	rheumatoid arthritis; CNS disorders; infection; metabolic disease;		
KW	cardiovascular disease; proliferative disorder; hormonal disorder;		
KW	neurological disorder; neuronal disorder; Alzheimer's disease; cancer;		
KW	attention deficit-hyperactivity disorder/attention deficit disorder;		
KW	Parkinson's disease; migraine; senile dementia; inflammatory disease;		
KW	rheumatoid arthritis; autoimmune disorder; respiratory ailment;		
KW	neuroprotective.		
OS	Homo sapiens.		
XX			
PL	WC200136473-A2.		
XX			
PD	25-MAY-2001.		
XX			
PF	16-NOV-2000; 2000WO-US31581.		
XX			
PR	16-NOV-1999; 99US-0165838.		
PR	17-NOV-1999; 99US-0166071.		
PR	19-NOV-1999; 99US-0166678.		
PR	28-DEC-1999; 99US-0173396.		
PR	22-FEB-2000; 2000US-0184129.		
PR	28-FEB-2000; 2000US-0185421.		
PR	28-FEB-2000; 2000US-0185554.		
PR	02-MAR-2000; 2000US-0186530.		
PR	03-MAR-2000; 2000US-0186811.		
PR	09-MAR-2000; 2000US-0188114.		
PR	17-MAR-2000; 2000US-0190310.		
PR	21-MAR-2000; 2000US-0190800.		
PR	20-APR-2000; 2000US-0198568.		
PR	02-MAY-2000; 2000US-0201190.		
PR	08-MAY-2000; 2000US-0203111.		
PR	25-MAY-2000; 2000US-0207094.		
XX			
PA	(PHAA ) PHARMACIA & UPJOHN CO.		
XX			
PI	Vogeli G, Wood LS, Parodi LA, Hiesch RR, Lind P, Slightom J;		
XX	Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;		
PI	WPI: 2001-389826/41.		
DR	N-PSDB; AAH51012.		
XX			
PT	New G protein-coupled receptor (ngPCR-x) and its encoding		
XX	polynucleotide useful for diagnosing and treating e.g. schizophrenia -		
PS	Claim 37; Pages 91-92; 261pp; English.		
XX			
CC	The present invention relates to novel G protein-coupled receptors		
CC	(ngPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,		
CC	28, 31-38, 40, 41, 53-60) and their coding sequences. The present		
CC	sequence is one such G protein-coupled receptor. GPCRs are also known as		
CC	seven transmembrane receptors and function in signal transduction. The		
CC	ngPCR coding sequences are useful for screening a human to diagnose a		

Query Match	Best Local Similarity	84.4%;	Score 1520;	DB 22;	Length 296;
Matches 286;	Conservative	0;	Mismatches 0;	Insertions 0;	Gaps 0;
QY 1 MFPCNNINISCVKNNKNSNDVRSALYSLSLAVLIITLVGNLVIYISIFKQLHPPTNML 60					
DB 2 mpfchmlhinscvkhmsndvrsalyslmvllliltlygnllivysishkqlheptnwl 61					
QY 61 IHSMATVDFLCLVWPYSNVRSAEHCWYEGEVPCKIHRSTQIMSSAIFPHLSFSDIR 120					
DB 62 IHSmatvdflllyclwmpysmvrseahcwyfgevfckihstsdimsasat'chlsfslidr 121					
QY 121 YVAVCDPLRYKAKKMLILYCVMIFFISWSYPAVFAFGMIFLELNTKGAEDILYKRVHVRGCG 180					
DB 122 YVavcdplrllyakakmlllylvcvmlffiswsypavfagfmfletnfgaeeilykvhvrcrg 141					
QY 181 GCVFPSKISGVTEFMTSPFIPGSIIMCVYRIRYLAKEDARLISDANQQLQGLEKKNCI 240					
DB 182 GcvfFskIsGvtelfmtsfyIpgsimcvyRirYlIakEqarIlSdanqkLIqglemngI 241					
QY 241 SOSKEKAAVKTIGIWMGVFLICMCPFCITVMDPFLHYIIPPLND 246					
DB 242 sGskErKavkLIgIwmGvflIcwcPfcItcvmDpflHyIIPpLnd 247					
RESULT 4					
IID AAB49231	standard: protein; 332 AA.				
XX AC AAB49231;					
XX DT 14-MAR-2001	(first entry)				
XX XX Rat SNORF33 receptor protein.					
KN SNORF33; inflammation; arthritis; neurological disorder; infection;					
KW bone disease; respiratory disorder; asthma; cancer; cardiovascular.					
OS Rattus rattus.					
XX PN WO200073449-A1.					
XX PD 07-DEC-2000.					
XX PF 26-MAY-2000; 2000WO-US14654.					
XX PR 28-MAY-1999; 99US-0322257.					
XX PR 06-OCT-1999; 99US-0413433.					
XX PA (SYNA-) SYNAPTIC PHARM CORP.					
XX PI Borowsky BE, Ogozalek KL, Jones KA;					
XX DR WPI, 2001-025252/03.					



OS Homo sapiens.  
 XX  
 XX WO200136473-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 16-NOV-2000; 2000MO-US31581.  
 XX  
 PR 16-NOV-1999; 99US-0165838.  
 PR 17-NOV-1999; 99US-0166071.  
 PR 19-NOV-1999; 99US-0166578.  
 PR 28-DEC-1999; 99US-0173396.  
 PR 22-FEB-2000; 2000US-0184129.  
 PR 28-FEB-2000; 2000US-0185421.  
 PR 28-FEB-2000; 2000US-0185554.  
 PR 02-MAR-2000; 2000US-0186530.  
 PR 03-MAR-2000; 2000US-0186811.  
 PR 09-MAR-2000; 2000US-0188114.  
 PR 17-MAR-2000; 2000US-0190310.  
 PR 21-MAR-2000; 2000US-0190800.  
 PR 20-APR-2000; 2000US-0198568.  
 PR 02-MAY-2000; 2000US-0201190.  
 PR 08-MAY-2000; 2000US-0203111.  
 PR 25-MAY-2000; 2000US-0207094.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J:  
 PI Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;  
 XX  
 DR WPI; 2001-389826/41.  
 DR N-PSDB; AAH51000.  
 PT New G protein-coupled receptor (ngPCR-x) and its encoding  
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -  
 XX  
 PS  
 XX  
 XX Claim 37; Page 86; 261pp; English.  
 CC The present invention relates to novel G protein-coupled receptors  
 CC (ngPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,  
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present  
 CC sequence is one such G protein-coupled receptor. GPCRs are also known as  
 CC seven transmembrane receptors and function in signal transduction. The  
 CC ngPCRx coding sequences are useful for screening a human to diagnose a  
 CC disorder affecting the brain or a genetic predisposition, specifically for  
 CC schizophrenia. ngPCRx are useful for identifying compounds useful for  
 CC treating schizophrenia. Detection of ngPCRx in a sample is useful as a  
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal  
 CC failure, rheumatoid arthritis, CNS disorders, infectious diseases such as HIV-1,  
 CC metabolic and cardiovascular diseases, proliferative disorders and  
 CC hormonal disorders. Modulators of ngPCRx activity have the utility for  
 CC treating neurological disorders, including schizophrenia, ADHD/ADD  
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),  
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,  
 CC migraine and senile dementia. Additional disorders include inflammatory  
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune  
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory  
 CC diseases e.g. inflammatory bowel disease.  
 CC  
 XX  
 XX Sequence 238 AA;

Query Match 67.0%; Score 1207; DB 22; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCHNINISCVKNNNSNDVRSALYSLMVLITTLVGNLIVIVSISHKQLHTPPNWL 60  
 |||||||  
 DB 11 mpfchniniscvknnsndvrsalyslmvlltltlvgnlivivsisfhkqlhtpcrwl 70  
 |||||||  
 QY 61 IHSNATVDFLLGCLVMPYSWVRSAEHGMVGEVCKIHTSTPDIIMLSASIFHLSFISDR 120  
 |||||||  
 DB 71 lhsnatvdfllgclvmpyswvrsaehegmvgvcklhtstpdilmssasifhsifsidr 130  
 |||||||

QY 121 YYAVCDPLRYKAKNNILVICMIFISWVPAVFAFGNIFLELNKGAEEIYKKHRCRG 180  
 |||||||  
 DB 131 yavcdplrykaknnilvicmifiswvpavfafgmflfelnkgaeclyknhvherg 190  
 |||||||  
 QY 181 CSVFESKISGVLTFMWSFYIPGSTMLCVYRIRYIAKEQARLISDANO 228  
 |||||||  
 DB 191 csvfesksigvltfmsfyipgsimlcvyryilylakegarllisdanq 238  
 |||||||

RESULT 7  
 AAB49230 standard; protein; 191 AA.  
 ID AAB49230  
 XX  
 XX AAB49230;  
 AC  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 XX Human SNORF33 receptor partial protein.  
 DE  
 XX  
 XX SNORF33; inflammation; arthritis; neurological disorder; infection;  
 KM bone disease; respiratory disorder; asthma; cancer; cardiovascular.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200073449-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 26-MAY-2000; 2000MO-US14654.  
 XX  
 XX 28-MAY-1999; 99US-0322257.  
 PR 06-OCT-1999; 99US-0413433.  
 XX  
 PA (SYNA-) SYNAPTIC PHARM CORP.  
 XX  
 XX Borowsky BE, Ogozalek KL, Jones KA;  
 PI  
 XX  
 DR WPI; 2001-025252/03.  
 XX  
 PT Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33  
 PT receptor which is useful for designing drugs for treating conditions  
 PT such as a chronic and acute inflammation, arthritis, neurological  
 PT disorders and microbial infections -  
 XX  
 XX  
 PS Disclosure; Fig 2; 227pp; English.  
 XX  
 XX The present invention relates to a mammalian SNORF33 receptor.  
 CC  
 CC SNORF33 antagonists and agonists are used to treat  
 CC abnormalities brought about by increased or decreased activity of the  
 CC mammalian SNORF33 receptor. The receptor is useful as a tool for  
 CC designing drugs for treating conditions such as a chronic and  
 CC acute inflammation, arthritis, neurological disorders, microbial  
 CC infections, bone diseases, respiratory disorders such as asthma,  
 CC cancers, cardiovascular disorders.  
 CC  
 XX  
 XX Sequence 191 AA;

Query Match 55.4%; Score 998; DB 22; Length 191;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-107;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 TVDFLLCLVMPYSWVRSAEHGMVGEVCKIHTSTPDIIMLSASIFHLSFISDRYAVC 125  
 |||||||  
 DB 1 tvdfllclvmpyswvrsaehegmvgvcklhtstpdilmssasifhsifsidryavc 60  
 |||||||  
 QY 126 DPLRYKAKNNILVICMIFISWVPAVFAFGNIFLELNKGAEEIYKKHRCRGCSVF 185  
 |||||||  
 DB 61 dplrykaknnilvicmifiswvpavfafgmflfelnkgaeeilyknhvrcrgscvff 120  
 |||||||  
 QY 186 SKISGVLTFMWSFYIPGSTMLCVYRIRYIAKEQARLISDANOQLQGLEKKNISQSK 245  
 |||||||

Dd	121 skisgvlcfmfsfyipgsmlcvyyriyliakegarllisdanqklqiglemknjsgske	180
Oy	246 RKAVKTLGIWM 256       	
Dd	181 rkavkltlgivm 191	
	RESULT 8	
AAAG72332	ID	AAAG72332 standard; Protein; 319 AA.
XX	AC	AAAG72332;
XX	DT	31-JUL-2001 (first entry)
DE	XX	Human OR-like polypeptide query sequence, SEQ ID NO: 2013.
XX	XX	Human; olfactory receptor; OR; primary scent determination;
KW	KW	secondary scent determination; polypeptide library; odour receptor;
KM	XX	scent profile; scent fingerprint; scent representation.
OS	XX	Homo sapiens.
PN	XX	WO200127158-A2.
PD	XX	19-APR-2001.
Pf	XX	06-OCT-2000; 2000MO-US27582.
PR	XX	08-OCT-1999; 99US-0158615.
PA	XX	24-FEB-2000; 2000US-0184809.
PA	(DIGI- ) DIGISCENTS.	
PA	(YEDA ) YEDA RES & DEV CO LTD.	
XX	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;	
PI	WPI: 2001-290713/30.	
DR	New polynucleotides which encode polypeptides involved in olfactory	
PT	sensation for identifying olfactory agonists and antagonists -	
PS	Example 6; Page 1350-1351; 1857pp; English.	
XX	The present sequence is a polypeptide encoded by one of 344 newly mined	
CC	human genes. It was used as a query sequence in a database search of	
CC	olfactory receptor (OR)-like sequences. The invention relates to isolated	
CC	polynucleotides encoding polypeptides involved in olfactory sensation.	
CC	The polynucleotides can be used in screening for olfactory agonists and	
CC	antagonists. The methods allow for the determination of primary scents	
CC	and the identification of the odour receptors used to detect these	
CC	primary scents. The methods also enable determination of secondary scents	
CC	and the identification of combinations of odour receptors that are	
CC	involved in detecting such secondary scents. This enables the	
CC	construction of a scent representation (also called a scent fingerprint	
CC	or scent profile), which may be used to re-create and edit scents.	
CC	Libraries of olfactory receptors are useful for determining the	
CC	interaction pattern of a composition with the receptors, and can be	
CC	used for determining differences in the olfactory faculties of different	
CC	individuals.	
XX	Sequence 319 AA:	
SQ		

Query Match	45.5%	Score 820	DB 22	Length 319
Best Local Similarity	47.5%	Pred. No. 1	6e-86	
Matches 153	Conservative 67	Mismatches 90	Indels 12	Gaps 4
QY	8	INISCKNNKMSNDYRA-----SLYSMLVILITLVLGNLIVYISISFKOLHPTWMLH	62	
Db	4	vnascdprn-----vripyswamyIvmIgisIvmtIvmIvmIstafkIsptrfII	58	
QY	63	SNATVFLLECLCLVMPYSMVNSAEHCWFGFVECKIHTSTDIMLSASIFLPLSFISIDRYX	122	

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Db 59 smaltidfllscvmpfvfvtitsiesocfygdalfckvhaccdilicttsifhnlcfvsard 118
OY 123 AVCDEPLRKAKMNIIIVCWMLEFMSQWPAVAFQFMILELNFGEAEFYKKNHYHRCGCS 182
Db 119 avxdqlgyctrlfpvdelffllmswspdliafgvfvsknlhgaee fvaaldcyglcv 177
OY 183 VFESKISCVLTFMTSFTYPSGIMLCVYRYRIYLAKEQARLISDANÖKLQIGLEKKNISQ 242
Db 178 llnfnpgvvaslafiaflpgettygilyhltivtarikhamqdygstrtkqgsseskwhp 237
OY 243 SK-ERRAKVETGIYWGVLICMCFEFICTVMDPLAHYIIPETLMDVLIMFGYLNSTENPM 301
Db 238 lkreskatrctlgivmgvfvclwlpbfvltlctdplinftecliedlyvflwlmgyfnsafnsi 297
OY 302 VYAFYFPMFERKALKMMLGKIF 323
Db 298 lgymlpymfwfkalrmlvtgmflf 319

```

XX	AAW35831	
XX	AAW35831 standard; Protein; 306 AA.	
XX		
XX	AAW35831;	
XX		
DT	27-FEB-1998 (first entry)	
XX		
DE	Human G protein conjugate type receptor.	
XX		
KW	Human; G protein; guanine nucleotide binding protein; gene therapy;	
KN	receptor ligand; genetic diagnosis.	
XX		
OS	Homo sapiens.	
XX		
PN	JP09238686-A.	
XX		
PD	16-SEP-1997.	
XX		
PF	07-MAR-1996; 96JP-0050678.	
XX		
PR	07-MAR-1996; 96JP-0050678.	
XX		
XX	(TAKE ) TAKEDA CHEM IND LTD.	
PA		
XX		
DR	WPI: 1997-506555/47.	
XX		
DR	N-PSDB; AAT94894.	
XX		
PT	Novel G protein conjugate receptor - used for identifying receptor	
PT	ligands which may potentially be useful in therapeutic drugs	
XX		
PS		
XX		
CC	Claim 1: Page 23-24; 31pp; Japanese.	
XX		
CC	The present sequence represents a G protein (guanine nucleotide-binding	
CC	protein) conjugate-type receptor protein. The G protein and its	
CC	encoding DNA are used in the development of a receptor-binding assay	
CC	system for screening for candidate drugs. The DNA and fragments of	
CC	it may also be used as primers or probes for genetic diagnosis, and	
CC	in gene therapy. The elucidation of the structure and properties of	
CC	the G protein conjugate-type receptor is expected to lead to the	
CC	development of unique drugs acting on its system.	
XX		
SQ	Sequence 306 AA.	

	Query Match	45.4%	Pred.	817:	DB 18;	length	306;
	Best Local Similarity	50.0%;	Score	No. 3,-e-86;			
	Matches 188;	Conservative	49;	Mismatches	85;	Indels	24; Gaps
OY	25 LYSLEWLLITTVGNILIVISLSRKHQLTTPNNLIHSMAFYDFLGLCLWPMSVRSRA	84					
	:     :	:	: :	:	:	:	:
Db	1 AYSFMGASFLTLTQLAMSLISSYKTKLPENPFIISMALDRLGITLTIMPYNMLTSRV	60					

```

QY      85  EHCYFEVCEKIKTITSDIMSSAIPHSIFSIDRYAACDPLRYAKANNIIVCIWF 144
Db      61  encyfyitlcklygsdmlstsisfhlsvaldrayacplystkltpikrll 120
QY      145  ISMSVPAVFAFGMIETLELNFGAEIYIKKHVHCRCGGSVFESKISGVLTEMTSPYIPGSI 204
Db      121  lcvswpafafgyvfaseayaadgieg-ydlivacasscpvfnfklwgtlflmagfflcpgsn 179
QY      205  MLCVYRYHYLIYAKROAQLISD--ANOKLOIGLEKKNISOSKSKKAKVTGTYMGVGLIC 262
Db      180  mvgilygkifavstrhahaimlengnqv-----kkckkaakklgiyivgvllic 229
QY      263  WCPEFICTVMDPEFLYLIIPPLANDVLIMFYGLNSTENPMVYAEFYEPVFRKALMMLEFGKI 322
Db      230  wfpcffctllldpflnfstypvllfcaaltwfygfnstcpllygffypfftralkylllqkl 289
QY      323  F-----QKDS 327
Db      290  fsaccfnltlcmqkes 305

```

RESULT	10
AA672401	
XX	AA672401 standard; Protein; 295 AA.
AC	
XX	AA672401;
DT	30-JUL-2001 (first entry)

DE Human OR-like polypeptide query sequence, SEQ ID NO: 2082.  
XX  
KW Human; olfactory receptor; OR; primary scent determination;  
KW secondary scent determination; polypeptide library; odour receptor  
KW scent profile; scent fingerprint; scent representation.

QS	Homo sapiens.
XX	
PN	WO200127158-A2.
XX	
PD	19-APR-2001.

PF	06-OCT-2000; 2000WO-US27582.
XX	
PR	08-OCT-1999; 990US-0158615.
PR	24-FEB-2000; 2000US-0184809.
XX	
PA	(DIGI-) DIGISCENTS.
PA	(YEDA) YEDA RES & DEV CO LT

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
XX  
DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory  
PT sensation for identifying olfactory agonists and antagonists -  
XX  
PS Example 6; Page 1396-1397; 1857pp; English.

CC The present sequence is a polypeptide encoded by one of 344 newly mined  
CC human genes. It was used as a query sequence in a database search of  
CC olfactory receptor (OR)-like sequences. The invention relates to isolated  
CC polynucleotides encoding polypeptides involved in olfactory sensation.  
CC The polynucleotides can be used in screening for olfactory agonists and  
CC antagonists. The methods allow for the determination of primary scents  
CC and the identification of the odour receptors used to detect these  
CC primary scents. The methods also enable determination of secondary scents  
CC and the identification of combinations of odour receptors that are  
CC involved in detecting such secondary scents. This enables the  
CC construction of a scent representation (also called a scent fingerprint  
CC or scent profile), which may be used to re-create and edit scents.  
CC Libraries of olfactory receptors are useful for determining the  
CC interaction pattern of a composition with the receptors, and can be  
CC used for determining differences in the olfactory faculties of different

CC	Individuals.
XX	
SO	Sequence

Query Match	45.2%;	Score 814.5;	DB 22;	Length 295;
Best Local Similarity	51.5%;	Pred. No. 6.1e-86;		
Matches 155;	Conservative 47;	Mismatches 86;	Indels 13;	Gaps 3;

OY 25 LYSMLVLIITLVGKLNIVYSISHEKOLHTPTNWLIIHSATVDLGLGYMPYSMSRSA 84  
::| | : | ::|||:|||||:| || |||||":||||:|  
Db 1 mysfmagsifitilfgnlamisisyfkqhltpcfnllismaitdfligftimpysmirsrv 60

[illegible]

Qy	Db	Qy	Db
205	180	263	230
MLCYVRYRLYLAKQARLISD--ANOKLTGLGLEKRNKINSOSKEKAAKTLGYAWGVFLIC	mvglygkifvavrskhahnamlnlenqny-----kkkkaakctlgivlygffllc	MCPEFFCTVMDPFLHLYIIPRLNVLVMEGTLNSTFNPVYAAFYAPYPRKRALMMLEPGKI	wfcfcctfcltlnlntscpvlltalcltwgyfntscpllllygltfllpffralkyylngkl
262	229	322	289

QY	323	F	32
Db	290	F	29

RESULT	11
AAW59907	
ID	AAW59907 standard; Protein; 343 AA

AC	AAW59907;
XX	
DT	20-NOV-1998 (first entry)

DE Human HNHC132 (G-protein coupled receptor).  
XX  
KW G-protein coupled receptor; HNHC132; agonist; antagonist; inhibition;  
KW bacterial infection; fungal infection; protozoan infection;  
KW viral infection.

OS	Homo sapiens.
XX	
PN	EP859055-A1.

PN	EP859055-A1.
XX	
PD	19-AUG-1998.

PD 19-AUG-1998.

PF 04-DEC-1997; 97EP-0309821.

24-JAN-1997; 97US-0788539.

XX  
PA (SMTK ) SMITHKLINE BEECHAM CORP.

PI Bergsma DJ, Sathe GM, Shabon U,

DR WPI; 1998-429683/37.  
DR N-PSDB; AAV41998Yq.

PT New polynucleotide encoding G-protein coupled receptor, used to prevent, treat and diagnose e.g., infections, pain, cancers, anorexia, asthma, Parkinson's disease, acute heart failure, hypertension, osteoporosis, ulcers and anxiety . . .

Claim 1; Fig 1; 23pp; English.

CC This is the nucleotide sequence of the novel G-protein coupled receptor





[illegible]

sq	Sequence	348 AA;
QY	Query Match	41.3%; Score 743; DB 21; Length 348;
Db	Best Local Similarity	42.5%; Pred. No. 1.5e-77;
Db	Matches 141; Conservative	63; Mismatches 126; Indels 2; Gaps 2;
QY	4	CHNIINISCVANNNSNDVRAISLSLMLVLLITLTVALNLIVISISHFQDLHPTWMLIHS 63
Db	14	cykhvnesckltpyspgprsllyavlaigfavlaafignllvmaalhfkqjhlptnfilas 73
QY	64	MATVDLLGCLVMPSPWRSRAEHCHVFEPEVCKHTITSDIMLSASIFLPSIDRYA 123
Db	74	lacedflvgvswmpstfvsvsvscwyigdsqclhtfcdfsfclsihlhccisvdrYA 133
QY	124	VCDDPLRYAKKNNILVICWIFISMSVPAVFAFGMIFLELNFKAEEIYYKHHHCRCGCSV 183
Db	134	vtqptltpckltvsvsgiclvswtfsvtsfysfsltygtaneeglaelvva-iltvvgcgqa 192
QY	184	FFSKISGVLTFMTSEFYIPGSIIMLCVYRYRIYLIAKBOARLISDANOKLOIGLEMKNGISOS 243
Db	193	plnqnvwtlfcfl-ffipnvamvflysklflvakhqarklaetlaeqagsseskyervak 251
QY	244	KERAAVLTGLIVMGVELICWCPEFICTYMDPLFIYIIPPTLNDVLIVHGYLNSTNPWY 303
Db	252	rerkaackltglamaaflvswlpylvdayldaymctfppvyvellowvllwcvyysamprly 311
QY	304	AFYPMWRKALKMMLFGKIRFOKDSRCLFLLE 335
Db	312	afiywvfgkaalkilvsgkvrltstnlfse 343

	RESULT	14
AAG80970		
ID	AAG80970	standard; Protein; 345 AA.
AC		
XX	AAG80970;	
DT	28-AUG-2001	(first entry)
DE	Human nGCR40 #2.	
XX		
KW	G protein-coupled receptor; nGCR; seven transmembrane-receptor;	
KW	signal transduction; schizophrenia; thyroid disorder; renal failure;	
KW	rheumatoid arthritis; CNS disorder; infection; metabolic disease;	
KW	cardiovascular disease; proliferative disorder; hormonal disorder;	
KW	neurological disorder; neuronal disorder; Alzheimer's disease; cancer	
KW	attention deficit-hyperactivity disorder/attention deficit disorder;	
KW	Parkinson's disease; migraine; senile dementia; inflammatory disease;	
KW	rheumatoid arthritis; autoimmune disorder; respiratory ailment;	
neuroprotective.		
XX		
OS	Homo sapiens.	
XX		
PN	WO200136473-A2.	
XX		
PD	25-MAY-2001.	
XX		
PF	16-NOV-2000; 2000MO-USJ3181.	
XX		
PR	16-NOV-1999; 99US-0165838.	
PR	17-NOV-1999; 99US-0166071.	
PR	19-NOV-1999; 99US-0166678.	
PR	28-DEC-1999; 99US-0173396.	
PR	22-FEB-2000; 2000US-0184129.	
PR	28-FEB-2000; 2000US-0185421.	
PR	28-FEB-2000; 2000US-0185554.	
PR	02-MAR-2000; 2000US-0186530.	
PR	03-MAR-2000; 2000US-0186811.	
PR	09-MAR-2000; 2000US-0188114.	
PR	17-MAR-2000; 2000US-0190310.	
PR	21-MAR-2000; 2000US-0190800.	
PR	20-APR-2000; 2000US-0198568.	



Tue Dec 11 16:12:40 2001

us-09-633-145-2.rag

Page 11

Search completed: December 11, 2001, 16:09:52  
Job time: 129 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 11, 2001, 16:08:44 : Search time 13.2 seconds  
(without alignments)  
938.842 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801  
Sequence: 1 MFCHNINISCVKNMNSND.....FGKIFOKDSSCKLFLLELS 338

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	542.5	30.1	388	5H4_CAVPO	O70528 cavia porce
2	539	29.9	388	5H4_MOUSE	P97288 mus musculu
3	534	29.7	388	5H4_HUMAN	Q13633 homo sapien
4	529	29.4	406	5H4_RAT	O62758 rattus norv
5	510.5	28.3	459	D1DR_FUGRU	P33452 fugu rubrip
6	497.5	27.6	465	D1DR_XENLA	P42291 xenopus lae
7	493.5	27.4	363	D1DR_CARAU	P35406 carassius a
8	492.5	27.3	358	HH2R_MOUSE	P97292 mus musculu
9	486	27.0	358	HH2R_RAT	P25102 rattus norv
10	481	26.7	457	DBDR_XENLA	P42290 xenopus lae
11	480	26.7	451	DADR_XENLA	P42289 xenopus lae
12	475	26.4	377	SH1D_RABIT	P49145 oryctolagus
13	474	26.3	377	SH1D_HUMAN	P28221 homo sapien
14	473	26.3	374	SH1D_RAT	P28565 rattus norv
15	472.5	26.2	359	HH2R_HUMAN	P25021 homo sapien
16	471	26.2	446	DADR_DIDMA	P42288 didelphis m
17	469	26.0	374	SH1D_MOUSE	O61224 mus musculu
18	467	25.9	446	DADR_PIG	P50130 sus scrofa
19	466.5	25.9	377	SH1D_CANFA	P11614 canis fami1
20	466.5	25.9	386	D1DR_OREMO	P47800 oreochromis
21	462.5	25.7	463	D5DR_FUGRU	P33452 fugu rubrip
22	461.5	25.6	376	SH1D_CAVPO	O60484 cavia porce
23	461	25.6	483	B1AR_MELGA	P07700 meleagris g
24	459.5	25.5	359	HH2R_CAVPO	P21728 cavia porce
25	458	25.4	446	DADR_HUMAN	P21728 homo sapien
26	457	25.4	446	DADR_MACMU	O77680 macaca mula
27	454.5	25.2	477	DBDR_HUMAN	P21918 homo sapien
28	453	25.2	385	B1AR_XENLA	O42574 xenopus lae
29	452.5	25.1	379	SH1D_FUGRU	P79748 fugu rubrip
30	452.5	25.1	418	B2AR_BOVIN	O28044 bos taurus
31	452	25.1	418	B2AR_MESAU	P04274 mesocricetu
32	451	25.0	418	B2AR_RAT	P10608 rattus norv
33	450.5	25.0	359	HH2R_CANFA	P17124 canis fami1

34	450	25.0	475	1	DBDR_RAT	P25115 rattus norv
35	449	24.9	418	1	B2AR_MOUSE	O18762 mus musculu
36	448	24.9	467	1	B1AR_BOVIN	O31916 bos taurus
37	446.5	24.8	415	1	B2AR_MACMU	O28509 macaca mula
38	446.5	24.8	446	1	DADR_RAT	P18901 rattus norv
39	446	24.8	466	1	B1AR_MOUSE	P34971 mus musculu
40	446	24.8	466	1	B1AR_RAT	P18090 rattus norv
41	445	24.7	467	1	B1AR_SHEEP	O28927 ovis aries
42	444.5	24.7	418	1	B2AR_FELCA	O28515 felis silve
43	444.5	24.7	468	1	B1AR_PIG	O28998 sus scrofa
44	443.5	24.6	415	1	B2AR_CANFA	P54833 canis fami1
45	443.5	24.6	474	1	B1AR_FELCA	O91626 felis silve

## ALIGNMENTS

RESULT	ID	5H4_CAVPO	STANDARD:	PRT:	388 AA.
AC	O70528:				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	5-HYDROXYTRYPTAMINE 4 RECEPTOR (5-HT4).				
DE	5-HYDROXYTRYPTAMINE 4 RECEPTOR (5-HT4).				
GN	HT4.				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.				
OX	NCBI_TaxID=10141;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Van den Wyngaert I., Gommers W., Jurzak M., Verhaaselt P., Gordon R.,				
RA	Leyden J., Luyten W., Bender E.;				
RT	"Cloning and expression of 5-HT4 receptor species and splice				
RT	variants.";				
RL	Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.				
CC	-1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR				
CC	5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC AMINE THAT FUNCTION				
CC	AS A NEUOTRANSMITTER, A HORMONE, AND A MITOCH. ACTIVITY OF				
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT S-FUNCTIONS ADENYLATE				
CC	CYCLASE (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY				
CC	ALTERNATIVE SPLICING.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: Y13585; CAA73912.1;				
DR	InterPro: IPR000276; GPCR_Rhodopsn.				
DR	Pfam: PF00001; 7tm.1; 1.				
DR	PRINTS: PR00237; GPCRHHODOPSN.				
DR	PRINTS: PR01059; 5HT4RECEPTR.				
DR	PRINTS: PR01103; ADRENERGICR.				
DR	PROSITE: PS00237; G-PROTEIN RECEPTOR F1.1; 1.				
DR	PROSITE: PS50262; G-PROTEIN RECEPTOR F1.2; 1.				
KW	G-protein coupled receptor; transmembrane; Glycoprotein;				
KW	Multiene family; Lipoprotein; Palmitate; Alternative splicing.				
KW	Extracellular; Intracellular; (POTENTIAL).				
FT	DOMAIN 1				
FT	TRANSSEM 20				
FT	TRANSSEM 41				
FT	DOMAIN 59				
FT	TRANSSEM 79				
FT	DOMAIN 80				
FT	TRANSSEM 94				
FT	TRANSSEM 117				
FT	DOMAIN 137				
FT	TRANSSEM 158				

FT DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 193 213 5 (POTENTIAL).  
 FT DOMAIN 214 260 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 261 281 6 (POTENTIAL).  
 FT DOMAIN 282 294 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 295 315 7 (POTENTIAL).  
 FT DOMAIN 316 388 CYTOPLASMIC (POTENTIAL).  
 FT CAROHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 93 184 BY SIMILARITY.  
 FT LIPID 329 329 PALMITATE (BY SIMILARITY).  
 SQ SEQUENCE 388 AA: 43725 MW: 304533A3/F60D02B CRC64.

Query Match 30.1%; Score 542.5; DB 1; Length 388;  
 Best Local Similarity 36.8%; Pred. No. 6e-28;  
 Matches 120; Conservative 57; Mismatches 128; Indels 21; Gaps 6;

QY 9 NISCVKNNMNDVSRASLVSLVLIITLVGNLIVVISISHRKOLH-TPPTNMLHSMATV 67  
 DB 7 NVSS-KEGGSVEKVLTLFLSAVILMALGNLVAVACRDRQLRKIKITNYFIYSLARA 65  
 QY 68 DDLGLGVPIYRYSVAEHCWTFGEVFCIKHSTDMSSASIFHLSTIDRYAV-CD 126  
 DB 66 DLVSVLVMPFGAIELVDIWIYGEWFCILVTSLDVLTASTFHLCCISLDRYAICQ 125  
 QY 127 PLRYAKNIIIVCMIFISMSVPAVAFAGMIFLELNFCAEETIKYKHVHCRCG---CS 182  
 DB 126 PLVYNNKMTPLIALMLGCGWCWYIPMFISLPIMGCHNNIGYDLIEKRFNONSSTYCV 185  
 QY 183 VEFSSISGLVTPMSTFYIPGSIIMLCVYRIYLIANEQARLISDANKIOIGLEMKNGISQ 242  
 DB 186 FMVNNPYALTCSVAFYIPELFLMLAVLAYRIYTAKEHAHQI---OVLQAGAPAGRPQ 241  
 QY 243 -----SKERAVKLGIVMGVFLICMCPFCITMDPELHIIPTPLNDVLIWNG 292  
 DB 242 PDDQSTHMRMRETKAAKLCITIMGCFCLCMAPFEVNTIDVPTDVTYVGLWTAFLWLG 301  
 QY 293 YLNSFTNPMVAVAFYFPPFKALKMML 318  
 DB 302 YINSGINPELVAFLNKSPFRAPFLIIL 327

RESULT 2  
 ID 5H4\_MOUSE STANDARD: PRT; 388 AA.  
 AC P97288; 089003; 089004; 09R2A4;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 5-HYDROXYTRYPTAMINE 4 RECEPTOR (5-HT-4) (SEROTONIN RECEPTOR) (5-HT4).  
 GN HT4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SWISS: TISSUE-Brain;  
 RX MEDLINE-97102706; PubMed-8946946;  
 RA Claeysen S., Sebden M., Journot L., Bockaert J., Dumuis A.;  
 RT "Cloning, expression and pharmacology of the mouse 5-HT(4L)  
 RT receptor";  
 RL FEBS Lett. 398:19-25(1996).  
 RN [2]  
 RP REVISIONS TO C-TERMINUS.  
 RA Dumuis A.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(B)).  
 RC STRAIN-SWISS: TISSUE-Brain;  
 RX MEDLINE-99127199; PubMed-9928238;  
 RA Claeysen S., Faye P., Sebden M., Taviaux S., Bockaert J., Dumuis A.;  
 RT "5-HT4 receptors: cloning and expression of new splice variants";

RL Ann. N.Y. Acad. Sci. 861:49-56(1998).  
 [4]  
 RN SEQUENCE FROM N.A. (ISOFORM 5-HT4(F)).  
 RP TISSUE-Brain;  
 RC MEDLINE-99238795; PubMed-10220570;  
 RA Claeysen S., Sebden M., Becamel C., Bockaert J., Dumuis A.;  
 RT "Novel brain-specific 5-HT4 receptor splice variants show marked  
 RT constitutive activity: role of the C-terminal intracellular domain";  
 RL Mol. Pharmacol. 55:910-920(1999).  
 CC -I- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR  
 CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION  
 CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF  
 CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
 CC CYCLASE (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -I- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 5-HT4(A), 5-  
 CC HT4(B) AND 5-HT4(F); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: Y09585; CAA70773.1; -  
 DR EMBL: Y09587; CAA70775.1; -  
 DR EMBL: Y09588; CAA70776.1; -  
 DR EMBL: AJ011369; CAA09598.1; -  
 DR GCRDB: GCR\_1315; -  
 DR MGD: MGI:109246; Htr4.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PRINTS: PR01059; 5HT4RECEPT.  
 DR PRINTS: PR01103; ADRENERGICR.  
 DR PROSITE: PS00237; G-PROTEIN-RECEP\_FL1; 1.  
 DR PROSITE: PS50262; G-PROTEIN-RECEP\_FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 19  
 FT TRANSMEM 20 40  
 FT DOMAIN 41 58  
 FT TRANSMEM 59 79  
 FT DOMAIN 80 93  
 FT TRANSMEM 94 116  
 FT DOMAIN 117 137  
 FT TRANSMEM 138 158  
 FT DOMAIN 159 192  
 FT TRANSMEM 193 213  
 FT DOMAIN 214 260  
 FT TRANSMEM 261 281  
 FT DOMAIN 282 294  
 FT TRANSMEM 295 315  
 FT DOMAIN 316 388  
 FT CAROHYD 7 7  
 FT DISULFID 93 184  
 FT LIPID 329 329  
 FT VARSPLIC 360 388  
 FT VARSPLIC 359 388  
 FT VARSPLIC 360 388  
 SQ SEQUENCE 388 AA: 43931 MW: F84163F39BA115B0 CRC64;

Query Match 29.9%; Score 539; DB 1; Length 388;  
 Best Local Similarity 36.0%; Pred. No. 1e-27;  
 Matches 113; Conservative 61; Mismatches 112; Indels 28; Gaps 6;



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FT LIPID 329 329 PALMITATE (BY SIMILARITY).
FT VARSPLIC 169 169 L-> LERSLNGLGODPHA (IN ISOFORM 5-
FT VARSPLIC 359 388 HT4(E)).
FT VARSPLIC 359 388 RDAVECGGOWESQCHPPTSPLVAAPSDT -> SGCSPVS
FT VARSPLIC 359 388 SELEFCNRPVPV (IN ISOFORM 5-HT4(E)).
FT VARSPLIC 359 388 RDAVECGGOWESQCHPPTSPLVAAPSDT -> SSGRETD
FT VARSPLIC 359 388 RNFGRIRRLTKPS (IN ISOFORM 5-HT4(D)).
FT VARSPLIC 360 388 DAVECGGOWESQCHPPTSPLVAAPSDT -> F (IN
FT VARSPLIC 360 388 ISOFORM 5-HT4(C)).
FT VARSPLIC 360 388 DAVECGGOWESQCHPPTSPLVAAPSDT -> YTVLARGH
FT VARSPLIC 360 388 HOELEKRLPHNDPESLESCF (IN ISOFORM 5-
FT VARSPLIC 360 388 HT4(A)).
SQ SEQUENCE 388 AA; 43761 MW; 7FCFEC60E7BDF560 CRC64;

Query Match 29.7%; Score 534; DB 1; Length 388;
Best Local Similarity 37.4%; Pred. No. 2,1e-27;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSIAVLITLTGNGLIYVISHKOLH-TPTNMLHSMATVDFLLGCLVWPSMVS 83
DB 22 LITFISTVLMAILGLWVAWAVCMCDROLKIKITNFIVSLAFADLLVSLVWPFQAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSASIFHLFSIDRYAV-CDPLRYAKNNILICYW 142
DB 82 VQDIWIYGEVFLVRSIDLVLITFTASIFHLCCSIDRYAICQPLVYNNKMTPLIALM 141
QY 143 ITISVSVPAVPAFGMIFELNFKGAEIYKHYHCRG-CSVFSKISGVLTMTSF 198
DB 142 LGGCAWYIPFISFLPMQNMNIGIIDLLEKRFNONSSTYCVFVWNPYATICSVAF 201
QY 199 YIPGSMICVYRYIYLAKEOARLISDANOKLOIGLEMNGISQS-----KERNA 248
DB 202 YIPELLMVAIYRIYTAKEHNOI-----QMLORAGASSESRQSDQSHTHMRPETA 257
QY 249 VKTGLVGVFLICWCFEFCITVMDPEFLHYIIPPLNDVLWFGVINSTFNWVAFPY 308
DB 258 AKTLCIMGCFICWAPFVTNIVDFIDYTVPGQWAFMLGVIYNSGLNPFLYAFUNK 317
QY 309 WFRKALKMML 318
DB 318 SFRRAFLLIT 327

RESULT 4
ID 5H4_RAT STANDARD: PRT; 406 AA.
AC 062758; 062757; 063006; 089034;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 5-HYDROXYTRYPTAMINE 4 RECEPTOR (5-HT-4) (SEROTONIN RECEPTOR) (5-HT4).
GN HTR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=95317299; PubMed=7796807;
RA Gerald C., Adam N., Kao H.T., Olsen M.A., Laz T.M., Schechter L.E.,
RA Bard J.A., Vaysse P., Hartig P.R., Branchek T.A., Weisshank R.L.;
RA "The 5-HT4 receptor: molecular cloning and pharmacological
RT characterization of two splice variants.";
RL EMOB J. 14:2806-2815(1995).
RN [2]
RP SEQUENCE OF 165-259 FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=95385798; PubMed=7656980;
RA Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RA "Expression of serotonin receptor mRNAs in blood vessels.";
RL FEBS Lett. 370:215-221(1995).

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RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(E)).
RC TISSUE=Brain;
RA MEDLINE=95238795; PubMed=10220570;
RA Claessen S., Sebben M., Becamel C., Bockaert J., Dumuis A.;
RA "Novel brain-specific 5-HT4 receptor splice variants show marked
RT constitutive activity: role of the C-terminal intracellular domain.";
RL Mol. Pharmacol. 55:910-920(1999).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: 5-HT4L (SHOWN HERE),
CC 5-HT4S AND 5-HT4(E) ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN BRAIN, THE 5-HT4S TRANSCRIPTS ARE
CC RESTRICTED TO THE STRIATUM, BUT THE 5-HT4L TRANSCRIPTS ARE
CC EXPRESSED THROUGHOUT THE BRAIN, EXCEPT IN THE CEREBELLUM. IN
CC PERIPHERAL TISSUES, DIFFERENTIAL EXPRESSION IS ALSO OBSERVED IN
CC THE ATRIUM OF THE HEART WHERE ONLY THE 5-HT4S ISOFORM IS
CC DETECTABLE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U20907; AAC52232.1; -
CC EMBL: U20906; AAC52232.1; -
CC EMBL: 248153; CAA88170.1; -
CC EMBL: AJ011370; CAA09599.1; -
CC DR GCRDB: GCR_1447; -
CC DR GCRDB: GCR_1448; -
CC DR GCRDB: GCR_1480; -
CC DR InterPro: IPR000276; GPCR_Rhodopsn.
CC DR Pfam: PF00001; 7tm_1; 1.
CC DR PRINTS: PR01059; 5HT4RECEPTR.
CC DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1.1; 1.
CC DR PROSITE: PS50262; G_PROTEIN_RECPEP_F1.2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.
CC MultiGene family; Alternative splicing; Lipoprotein; Palmitate.
CC -----
CC DOMAIN 1 19
CC FT DOMAIN 1 19
CC FT TRANSMEM 20 40
CC FT DOMAIN 2 41 58
CC FT TRANSMEM 59 79
CC FT DOMAIN 80 93
CC FT TRANSMEM 94 116
CC FT DOMAIN 117 137
CC FT TRANSMEM 138 158
CC FT DOMAIN 159 192
CC FT TRANSMEM 193 213
CC FT DOMAIN 214 260
CC FT TRANSMEM 261 281
CC FT DOMAIN 282 294
CC FT TRANSMEM 295 315
CC FT DOMAIN 316 406
CC FT CARBOHYD 7 7
CC FT DISULFID 93 184
CC FT LIPID 329 329
CC FT VARSPLIC 360 406
CC FT VARSPLIC 359 406
CC FT CONFLICT 74 75
CC FT SEQUENCE 406 AA; 46107 MW; A1889155A08930B4 CRC64;

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Query Match 29.4%; Score 529; DB 1; Length 406;  
 Best Local Similarity 35.4%; Pred. No. 4.5e-27;  
 Matches 11; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

25 LYSIMVLIITLTVGNLIVIVSISHFQKQLH-TTPNMLIHSMAVDFLLGCLVMPYSNVR 83  
 22 LITFFAVVIMAILGNLVAACRDRQLRKIKITNFIYSIAFLDVLVSVNAFGAIEL 81  
 84 AEHWYGEVEFKIHTSTDMILSSASIFHLSTSIDRYAV-CDPLRYKAKMNLIVICVM 142  
 82 VQDIWFGEHFCVLRISDLVLTLTASIFHLCSIDRYAACCPPLVYRNKMTPLRLTALM 141  
 143 IFTSMSPAVPARGMIFLELNFKAEBITY---KHHVCRGGSVFESKISGVLTMTSF 198  
 142 LGGCVWVPMFISFLPIQGNMNIIVDIEKRKHNSNSTFCVEMVKNKPYATICSVAIF 201  
 199 YIGSIMLCVYRYRYLAKQARLISDANKLOIGLEMKNISGSK----- 244  
 202 YITPLMVLVLYRYRYVAKHA-----QOIQM-IDPAGATSSRQTDADONSTHMRMT 253

245 ERKAKTGLIVMGVFLICMCPFFICTYMDPLATIIPTLNDVLIMFGYLNSTFNPMVYA 304  
 254 ETRAKTKLCVIMGCFCCCMARPEFYTNIVDPIDYVEKWTATLWLGYNGLNPLIYA 313  
 305 FFFYWERKALKMML 318  
 314 FLNKSFRRAFLIL 327

RESULT 5  
 DDIR\_FUGRU STANDARD; PRT; 459 AA.  
 ID DDIR\_FUGRU  
 AC P53452;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE D(1)-LIKE DOPAMINE RECEPTOR.  
 GN D14.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Petcomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95309911; PubMed=7789977;  
 RA Machae A.D., Brenner S.;  
 RT "Analysis of the dopamine receptor family in the compact genome of  
 the puffer fish Fugu rubripes.";  
 RL Genomics 25:436-446(1995).  
 CC -!- FUNCTION: RECEPTOR FOR DOPAMINE.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: X80174; CAA56455.1; -.  
 CC HSSP: P29274; 1MMH.  
 CC GCRDB: GCR\_1108; -.  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHDOPSN.  
 CC PRINTS: PR00242; DOPAMINER.  
 CC PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
 CC PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.  
 CC PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 MultiGene Family.  
 FT DOMAIN 1 23  
 FT TRANSSEM 24 49  
 FT DOMAIN 50 60  
 FT TRANSSEM 61 87  
 FT DOMAIN 88 96  
 FT TRANSSEM 97 119  
 FT DOMAIN 120 138  
 FT TRANSSEM 139 164  
 FT DOMAIN 165 191  
 FT TRANSSEM 192 216  
 FT DOMAIN 217 269  
 FT TRANSSEM 270 297  
 FT DOMAIN 298 311  
 FT TRANSSEM 312 333  
 FT DOMAIN 334 459  
 FT CARBOHYD 4 4  
 FT DISULFID 96 187  
 SQ SEQUENCE 459 AA; 51080 MW; B69857A3A4E10B CRC64;

Query Match 28.3%; Score 510.5; DB 1; Length 459;  
 Best Local Similarity 37.0%; Pred. No. 7.2e-26;  
 Matches 118; Conservative 54; Mismatches 110; Indels 37; Gaps 8;

31 LIITTVGNLIVIVSISHFQKQLH-TTPNMLIHSMAVDFLLGCLVMPYSNVRSAEHCMY 89  
 32 LIITFTLGNLTVCAVAVYKFRHLRSKVTNFFVLSAISDLVALLVWMAKATEIMGWP 91  
 90 FGEVFCIKIHTSDIMLSSASIFHLSTSIDRYAVCDPLRYKAKMNLIVICMFIKNSV 149  
 92 FGE-FCNIMVAFDIMCSASTILNCVISTVDRYMAISSPFYERKMTPEVACIMISVATL 150  
 150 PAVFAFGMIFLELNFKAKEELIYKHHVHORG-----GGSVFESKISGVLTMTSFYI 200  
 151 SVLSF--IPVQLWMMKRAQTASY--VELNGTYAGDLPDNCDSLNRYAISSSLISFYI 206  
 201 PGSIMLCVYRYRYLAKQARLI-----SDANKLOIGLEMKNGISOSKER 246  
 207 PVALIMVITHTIYRRAQOIRISALERAESAQRNHSMSNGSLMESECFKMSFKRET 266  
 247 KAVTGLIVMGVFLICMCPFFICTYMDPLATIIPTLNDVLIMFGYLNSTFN 299  
 267 KVLKTLVIMGVFVCCWPFELNCMVFCEDADTTPDPCISSTFDVFEVFGMANSLSL 326

300 PMVAFEFYWERKALKMML 318  
 327 PITYAFNAD-FRKAFSTIL 344

RESULT 6  
 DCDR\_XENLA STANDARD; PRT; 465 AA.  
 ID DCDR\_XENLA  
 AC P42291;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE D(1C) DOPAMINE RECEPTOR.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95024150; PubMed=7937989;  
 RA Sugamori K.S., Demchyshyn L.L., Chung M., Niznik H.B.;  
 RT "D1A, D1B, and D1C dopamine receptors from Xenopus laevis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10536-10540(1994).  
 CC -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS  
 CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC or send an email to license@sdb.ch).
-----
DR EMBL: U07865; AAA50830.1; -.
DR HSSP: P29274; 1MMH.
DR GCRDB: GCR_1236; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00242; DOPAMINER.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1 54 1 (POTENTIAL).
FT DOMAIN 55 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 92 2 (POTENTIAL).
FT DOMAIN 93 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 124 3 (POTENTIAL).
FT DOMAIN 125 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 168 4 (POTENTIAL).
FT DOMAIN 169 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 219 5 (POTENTIAL).
FT DOMAIN 220 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 291 6 (POTENTIAL).
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 334 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 335 465 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 187 BY SIMILARITY.
FT LIPID 344 344 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 465 AA; 52640 MW; F4IDF85AE0D2P869 CRC64;

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Query Match 27.6%; Score 497.5; DB 1; Length 465;
Best Local Similarity 34.5%; Pred. No. 4.8e-25;
Matches 118; Conservative 61; Mismatches 130; Indels 33; Gaps 8;

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QY 6 NIINISCVKNNMSND-----VRASYSLMVLIIITLGNLITVIVSISHFKQLHNP 56
DB 5 SIFENTV--NWVHADLDVGNDSLRLALGLLSLILSLITLGNLITVCAVTKFRLLRSK 62
QY 57 -TNWLIHSNATVDFLLGLVMPYSNVSRAHCWYGFGEVCKIHTSTDMLSASIFHLSP 115
DB 63 VTNFVSIASVSDLEFVALLVPMKAVTEVAGFWFGD-FCDTWVAFDIDICSTASILNLCI 121
QY 116 ISIDRYVAVCDPLRKAKKNILVICMIFISVPAVAFGFIPLINKGABEITYKAV 175
DB 122 ISLDRTVMAISPERYERKTKQVAFIMIGVANTLSLISFIVQSWHSHADELNGV 181
QY 176 HCRGGSVFEFSKISGVLTFMSTFIPGSIIMCVYRIYLIKQARLISDAN-----OK 229
DB 182 NHTENCDSLNRTVTAISSLSIFILPVYIMITRITRIYIAQTQIRRISSLERAVHAOR 241
QY 230 LQIGLEKNGISQ--KERRAKVTLGIWGVFLICWCPEFFICTVADPELHYIIP----- 281
DB 242 CSSRLSNENSKTSERKTKYVLTSLIMGVFCMLPFEVLNCMIPLFCMMLPGQNEPE 301
QY 282 -----PLINDVLIWFGYLNSTFNPNVYAFYFWFKALKML 318
DB 302 PCVSETTFNIFWFGMANSSLNPIVYAFNAD-FRKAFTTIL 342

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RESULT 7
DIDR_CARAU STANDARD: PRT; 363 AA.
AC P35406;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE D(1) DOPAMINE RECEPTOR.
OC Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoplethyeri; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94088471; PubMed=8264547;
RA Frail D.E., Manelli A.M., Witte D.G., Lin C.W., Steffey M.E.,
RA Mackenzie R.G.;
RT "Cloning and characterization of a truncated dopamine D1 receptor
RT from goldfish retina: stimulation of cyclic AMP production and
RT calcium mobilization."
RL Mol. Pharmacol. 44:1113-1118(1993).
CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE. COULD BE INVOLVED IN
CC GROWTH HORMONE RELEASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: RETINA.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL: L08602; AAA16322.1; -.
DR HSSP: P29274; 1MMH.
DR GCRDB: GCR_0525; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00242; DOPAMINER.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 45 1 (POTENTIAL).
FT DOMAIN 46 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 81 2 (POTENTIAL).
FT DOMAIN 82 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 164 4 (POTENTIAL).
FT DOMAIN 165 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 271 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 272 297 6 (POTENTIAL).
FT DOMAIN 298 310 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 311 330 7 (POTENTIAL).
FT DOMAIN 331 363 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 97 187 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 363 AA; 40651 MW; 4B47DE240D65DD0 CRC64;

```

Query Match

27.4%; Score 493.5; DB 1; Length 363;

Best Local Similarity 36.3%; Pred. No. 7.1e-25;  
Matches 118; Conservative 59; Mismatches 117; Indels 31; Gaps 8;

```
QY 21 VRASISLWVLIITLTGNLIVIVSISHPKQLHPR-TNMLIHSMATVDLLGCLVMPYS 79
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 23 VRLTGLSFLVLIITLTGNLIVIVSISHPKQLHPR-TNMLIHSMATVDLLGCLVMPYS 82
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 80 MVRSAEHCVGEVECKIHTSTDMLSASIFHLFSIDRYAADCPLRYKAKNIIIVY 139
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 83 AVTEVAGWPGG-AECDLWAFADIMCSTASILNLCVSDRWALSSPFRYERKMTPEVA 141
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 140 CVMIFISVPAVAFGMIFELNFKGAEEIYKHVHC-----RGCSVFEKISGVLT 193
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 142 FVMISGATLTLVLSIF--IPVQLKWKHAKQPIGFLFNASRRDLPDNCDSILRTYAIS 199
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 194 FMTSYFISGIMLCVYRYIYLAKQARLIS--DANOKLOI-----GLEMKNG 239
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 200 SLISFYIYVIMIVTYTYIYRIAKQIRISALERAESAQIRHDSMGSGNMDESSFK 259
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 240 ISQSKERRAVTGLIVMGVFLICMCPFFICVMDPFLHY-----IIPPTLVLMFGY 293
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 260 LSKRETKVLTLSIVMGVFLICMCPFFICVMDPFLHY-----IIPPTLVLMFGY 319
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 294 LNSTFNPVAVAFEFYPMFKALKMML 318
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 320 ANSSLNPITVAFNAD-FRRFAFALL 343
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
```

RESULT 8  
HH2R\_MOUSE STANDARD; PRT; 358 AA.

```
AC P97292;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HISTAMINE H2 RECEPTOR (H2R) (GASTRIC RECEPTOR 1).
GN HRH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA;
RX MEDLINE=97092891; PubMed=8938453;
RA Kobayashi T., Inoue I., Jenkins N.A., Gilbert D.J., Copeland N.G.,
   Watanabe T.,
   "Cloning, RNA expression, and chromosomal location of a mouse
   histamine H2 receptor gene."
RL Genomics 37:390-394(1996).
CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
   ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
   PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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```

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CC -----
DR EMBL: D50096; BAA08792.1; -
DR GCRDB: GCR1155; -
DR MGI: MGI:108482; Hrn2.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00531; HISTAMINEH2R.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
```

```
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22
FT TRANSMEM 23 44
FT DOMAIN 45 57
FT TRANSMEM 58 81
FT DOMAIN 82 92
FT TRANSMEM 93 114
FT DOMAIN 115 134
FT TRANSMEM 135 159
FT DOMAIN 160 179
FT TRANSMEM 180 203
FT DOMAIN 204 233
FT TRANSMEM 234 257
FT DOMAIN 258 266
FT TRANSMEM 267 288
FT DOMAIN 289 358
FT SITE 98 98
FT SITE 185 185
FT SITE 189 189
FT SITE 189 189
FT CARBOHYD 4 4
FT DISULFID 91 173
FT SEQUENCE 358 AA; 40379 MW; D3DBA81D71B6D927 CRC64;
SQ
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Query Match 27.3%; Score 492.5; DB 1; Length 358;  
Best Local Similarity 35.0%; Pred. No. 8.2e-25;  
Matches 115; Conservative 54; Mismatches 111; Indels 49; Gaps 7;

```
QY 30 VLIITLTIV-----GNLIYVSIHFKQLATPTNMLIHSMATVDLLGCLVMPYSNVRSA 84
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 21 ISVLTTLTIFIVAGVAVVCLAVSLNRRRLSLNCFIVSLAATDGLLVMPFSAIYQL 80
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 85 EHCWFGVEVECKIHTSTDMLSASIFHLFSIDRYAADCPLRYKAKNIIIVY 144
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 81 SEKMRFGVEVECKIHTSTDMLSASIFHLFSIDRYAADCPLRYKAKNIIIVY 140
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 145 ISMSVPAVAFGMIFELNFKGAEEIYKHVHCGRG-----CSVFEKISGVLTFTPSFY 199
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 141 FIMVISTLISFLSIHLGWSNRNG-----TRGNDTFKCKVQVNEYVGLVDGWTY 191
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 200 IFSIMLCVYRYIYLAKQARLISDANOKLOIGLEMKNGISOSK-----ERKAVTTIGI 254
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 192 LPLLIMCVYRYIYLAKQARLISDANOKLOIGLEMKNGISOSK-----ERKAVTTIGI 237
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 255 VMGVFLICMCPFFICTVM-----DPFLHYIIPPTLVLMFGYLNSTFNPVAVAFYTP 308
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 238 VMGVFLICMCPFFICTVM-----DPFLHYIIPPTLVLMFGYLNSTFNPVAVAFYTP 292
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 309 WFRKALKMMLFGKIPKODSSROCKFELS 337
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 293 DFRMAYQQLFHCKLASHNSHKTSRLRINS 321
    || :|||:||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
```

```
RESULT 9
HH2R_RAT STANDARD; PRT; 358 AA.
AC P25102;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HISTAMINE H2 RECEPTOR (H2R) (GASTRIC RECEPTOR 1).
GN HRH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92028890; PubMed=1930188;
```

RA Rut M., Traifort E., Arrang J.-M., Leurs R., Schwartz J.-C.;  
 RT "Cloning and tissue expression of a rat histamine H2-receptor gene";  
 RL Biochem. Biophys. Res. Commun. 179:1470-1478(1991).  
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC  
 CC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: S57565; AAB19935.1; -  
 DR PIR: J01278; J01278.  
 DR GCRDB: GCR\_0308; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PRINTS: PR00531; HISTAMINEH2R.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 22  
 FT TRANSMEM 1 22  
 FT DOMAIN 23 44  
 FT TRANSMEM 45 57  
 FT DOMAIN 58 81  
 FT TRANSMEM 82 92  
 FT DOMAIN 93 114  
 FT TRANSMEM 115 134  
 FT DOMAIN 135 159  
 FT TRANSMEM 160 179  
 FT DOMAIN 180 203  
 FT TRANSMEM 204 233  
 FT DOMAIN 234 257  
 FT TRANSMEM 258 266  
 FT DOMAIN 267 288  
 FT TRANSMEM 289 358  
 FT SITE 98  
 FT SITE 185  
 FT SITE 185  
 FT SITE 189  
 FT SITE 189  
 FT CARBOHYD 4 4  
 FT DISULFID 91 173  
 FT SEQUENCE 358 AA; 40253 MW; 4886F69B7B5DDDC CRC64;

Query Match 27.0%; Score 486; DB 1; Length 358;  
 Best Local Similarity 34.0%; Pred. No. 2, 1e-24;  
 Matches 117; Conservative 56; Mismatches 123; Indels 48; Gaps 7;

OY 245 -----ERKAVKTLGVKGVFLICWCPFICTVMDPFLHY-----11PPTLNDVLWFGY 293  
 DB 224 ATRREKATVTLAAVACAFITCFFPTFAV-----YRLRDDDAINEAVEGIVLMGY 277  
 OY 294 LNSTFNPVYAFEPYPERKALKMFLGKIPKDKSSRCKFLFELS.337  
 DB 278 ANSALNPILYAAINRDPRTAYQDLFCKFASHSHSKTSRLNNS 321  
 RESULT 10  
 ID DBDR\_XENLA STANDARD; PRT; 457 AA.  
 AC P42290;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE D(1B) DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR).  
 OS Xenopus laevis (African clawed frog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95024150; PubMed-7937989;  
 RA Sugamori K.S., Demchishyn L.L., Chung M., Niznik H.B.;  
 RT "D1A, D1B, and D1C dopamine receptors from Xenopus laevis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10536-10540(1994).  
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1, D2, D3, D4, D5) OF RECEPTORS  
 CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: BRAIN AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: U07864; AAA50829.1; -  
 DR HSSP: P29274; 1MAH.  
 DR GCRDB: GCR\_1321; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PRINTS: PR00242; DOPAMINER.  
 DR PRINTS: PR00566; DOPAMINED1B.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Multigene family; Lipoprotein; Palmitate.  
 FT DOMAIN 1 41  
 FT TRANSMEM 42 67  
 FT DOMAIN 68 78  
 FT TRANSMEM 79 105  
 FT DOMAIN 106 114  
 FT TRANSMEM 115 137  
 FT DOMAIN 138 156  
 FT TRANSMEM 157 181  
 FT DOMAIN 182 205  
 FT TRANSMEM 206 231  
 FT DOMAIN 232 282  
 FT TRANSMEM 283 309  
 FT DOMAIN 310 326  
 FT TRANSMEM 327 351  
 FT DOMAIN 352 457  
 FT CARBOHYD 24 24  
 FT DISULFID 114 199  
 FT SEQUENCE 457 AA; 10253 MW; 4886F69B7B5DDDC CRC64;

FT	LIPID	SEQUENCE	361	361	PALMITATE (BY SIMILARITY).
50	SEQUENCE	457 AA; 51656 MW; A0A389311E4CD2EB	CNC64;		
	Query Match	26.7%; Score 481; DB 1; Length 457;			
	Best Local Similarity	35.5%; Pred. No. 5,3e-24;			
	Matches 113; Conservative 54; Mismatches 121; Indels 30; Gaps 7;				
QY	27	SLMWLIITLVGLNLIIVISISHEKQLT-PTNMLIHMATVDFLLGLVMPYSNRSAE 85			
Db	46	SLLLLIITLVGLNLIIVCTAVMRFRHLSRVTNPIFVSLAVSDLLVALLVMPKAAVEVA 105			
QY	86	HCWYRGEVFCIKHSTDTMLSSAFHLSFISIDRYAVCPRLKAKMNIIVCMFI 145			
Db	106	GHWPEG-AFCDIWAFFDLMCTASTLNLCTVSDVYMAISSPFREKMTORFVALLTST 164			
QY	146	SWSYVAFVAFGMIFELNLF-KGAEIYYKHHNRCGSCVFSKIGVLTFTMFTSFIYPSI 204			
Db	165	AWALSVLISF--IPQLSMHKSSETDHLNHSITGNCSSLNRTYATISSLSIFIIPAI 222			
QY	205	MLCVYRYIYIAKEQARLLISDANKLQIGLEMKNG-----ISQSKERRAKV 250			
Db	223	MIWYTRIRYIAQIDIKRKISTLERAAEHAQSCRNSRNVDCSRHHOTSLRTSIKKETVVK 282			
QY	251	TLGIVMGVFLIWCFFICTYVMDPLAH-----IIPPTLVLYLWGYLSTNPNP 300			
Db	283	TLTIIMGVYCCWLPFFELINCMVPPCDRSPGHPOAGLPCVSETPTDIFVFGMANSIDNP 342			
QY	301	MYVAFYPMFPRKALKMML 318			
Db	343	IIVAFNAD-FKRVFSSLL 359			
RESULT	11				
ID	DADR_XENLA	STANDARD:	PRT:	451 AA.	
AC	P42289;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	01-NOV-1995 (Rel. 32, Last annotation update)				
DE	D(1A) DOPAMINE RECEPTOR.				
OS	Xenopus laevis (African clawed frog).				
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8335;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-95024150; PubMed-7937989;				
RA	Shigemori K.S., Demchyshyn L.L., Chung M., Niznik H.B.;				
RT	"D(1A), D1B, and D1C dopamine receptors from Xenopus laevis.,"				
RL	Proc. Natl. Acad. Sci. U.S.A. 91:10536-10540(1994).				
CC	-1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: BRAIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	-----				
DR	EMBL; U07863; AAA50828.1; -.				
DR	HSSP; P29274; IMMH.				
DR	GCRRDB; GCR.1398; -.				
DR	InterPro; IPR000276; GPCR_Rhodopsn.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PR00237; GPCRHHODOPSN.				

DR	PRINTS: PR000242; DOPAMINER.
DR	PRINTS: PS00365; DOPAMINER.
DR	PROSITE; PS00237; G-PROTEIN_RECPEP_F1.1; 1.
DR	G-PROTEIN; PS00262; G-PROTEIN_RECPEP_F1.2; 1.
KV	MultiGene family: Lipoprotein; Palmitate.
KW	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 1 22
FT	TRANSMEM 23 48
FT	DOMAIN 49 59
FT	TRANSMEM 60 86
FT	DOMAIN 87 95
FT	TRANSMEM 96 118
FT	DOMAIN 119 137
FT	TRANSMEM 138 162
FT	DOMAIN 163 191
FT	TRANSMEM 192 217
FT	DOMAIN 218 271
FT	TRANSMEM 272 298
FT	DOMAIN 299 315
FT	TRANSMEM 316 340
FT	DOMAIN 341 451
FT	CARBOHYD 4 4
FT	DISULFID 95 185
FT	LIPID 350 350
SQ	SEQUENCE 451 AA; 50549 MM; 3A0FA8B36C166687 CNG64;
Query Match 26.7%; Score 480; DB 1; Length 451;	
Best Local Similarity 34.5%; Pred. No. 6e-24; "	
Matches 111; Conservative 56; Mismatches 117; Indels 38; Gaps 7;	
OY	31 LIILTLTVGNLIVVISISHFKQLHTP-TNMLIHSATYDFELGLCLVMPEYSNVRSRSGCWY 89
DB	31 VLLITSLTGLNTLCVAALIRFRRLRSKVTNFVFISLAVSDLLVALVLMPMKVAELAGFWP 90
OY	90 FGEVCKIHSTSDIMLSASIFHLSFISIDRYAACDLBRKAKNNILVICMFIEMSV 149
DB	91 FG-TGCNIWVARDINCSPASILNLGVISDRYWLAISSPRERKKTPPVAFIMIGVANTL 149
OY	150 PAVFAFGMIETLEANKGAEEIYY-----KNHCRCGGSVFSKISGYLTFTMSFYIGS 203
DB	150 SYLVISF--IPVOLNMHKAKKTTSFPDLNTLHDRTMDNCDSLNRIFYALLSYLIPIYA 207
OY	204 IMLCVYRIYLIAKEDARLISDANOKLOIGEMKNGISO-----SKER 246
DB	208 IIIVTYTRIYRIAQAQRISALSERAAYNAKMCNSTSNRNSLDCCQPESLSIKTSFKRET 267
OY	247 KAVKLGIYMGVEFLCMCFEFICYMDPLH-----YIIPPLNDVLIMNGYINS 296
DB	268 KYVKLTLSYMGVFCWCMLPEFLINCIVPCDPSLTTSGETPCISSITYEDFVWFEGMANS 327
OY	297 TENPMUYAEFYPPFRKALKML 318
DB	328 SLNPITIIYAFNAD-FRKAPSNLL 348
RESULT 12	
SHID_RABIT	
ID SHID_RABIT STANDARD: PRT: 377 AA.	
AC P49145; 002823; Rel. 33, Created)	
DT 01-FEB-1996 (Rel. 33, Last sequence update)	
DT 01-FEB-1996 (Rel. 33, Last annotation update)	
DT 15-JUL-1998 (Rel. 36, Last annotation update)	
DE 5-HYDROXYTRYPTAMINE 1D RECEPTOR (5-HT-1D) (SEROTONIN_RECEPTOR)	
DE (5-HT-1D-ALPHA).	
GN HTR1D.	
OS Oryctolagus cuniculus (Rabbit).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
OX NCBI_TaxId=9986;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Liver;	

```

RX MEDLINE=96130324; PubMed=8543023
RA Harwood G.S., Lockyer M., Giles H., Fairweather N.;
RT "Cloning and characterization of the rabbit 5-HT1D alpha and 5-HT1D
RL beta receptors."
RN FEBS Lett. 377:73-76(1995).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RA MEDLINE=97032156; PubMed=8878052;
RX Bard J.A., Kucharewicz S.A., Zgonibick J.M., Weinschank R.L.,
RA Branchek T.A., Cohen M.L.;
RT "Differences in ligand binding profiles between cloned rabbit and
RN human 5-HT1D alpha and 5-HT1D beta receptors: ketanserin and
RP methiothepin distinguish rabbit 5-HT1D receptor subtypes."
RL Naunyn Schmiedeberg Arch. Pharmacol. 354:237-244(1996).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLYLATE
CC CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
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CC or send an email to license@isb-slb.ch).
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CC
DR EMBL; Z50162; CAA90530.1; -;
DR EMBL; U60825; AAB58466.1; -;
DR GCRDB; GCR.1293; -;
DR GCRDB; GCR.1577; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1_1; 1.
DR PRINTS; PRO0237; GPCR RHODOPSIN.
DR PRINTS; PRO0514; 5HT1D RECEPTOR.
DR PRINTS; PRO1101; 5HT RECEPTOR.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL.1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECPT_FL.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
KW
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 62 1 (POTENTIAL).
FT DOMAIN 63 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 98 2 (POTENTIAL).
FT DOMAIN 99 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 134 3 (POTENTIAL).
FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 176 4 (POTENTIAL).
FT DOMAIN 177 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 218 5 (POTENTIAL).
FT DOMAIN 219 302 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 303 326 6 (POTENTIAL).
FT DOMAIN 327 335 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 336 360 7 (POTENTIAL).
FT DOMAIN 361 377 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 5 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHD 17 17 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHD 21 21 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT DISULFD 111 188 BY SIMILARITY.
FT CONFLICT 28 A -> I (LIN REF. 2).
SO SEQUENCE 377 AA; 41500 MW; FCL441678AB82B0A CRC64;

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Dd      37 LKISLAVALSTIVATVFNSTFNFVLTTILLTRKLHPANVLGSLATPTDLVSILWPISTI   96
Qy      81 VRSACHCVFGFEVFPEKIHITSDIMLSASIFLSEISIDRYAYACDPTRYAKNNILVIC   140
Db      97 AVTIHTHNFQGVCLDIWSSSDITCCTASILHLCAIALDRWAITDALEYSKRRRAGMAA   156
Qy     141 VMIFISVSPAVFAFCMIFLELNFKGADEIYYKHVCNGGCSVPFSKTS-GYLTPMTSFY   199
Db     157 AMIAVVAMIASICISIPPLFWR-QAKAAHEV-----SDCLVNNTSQISTYITSYGAFY   207
Qy     200 IPGSIMLCVYRIYILAEO-----ARLSIDA-----                226
Db     208 IPSVLLIYLGITYMAANNRLINPSSLGKRFTTAHLITGSAGSSGLSBSLGEGSHS    267
Qy     227 -----NOKLOIGEMKNGISOSKERKRAVKTLGYVMGFLLCMOPFFICYTMDPFL    276
Db     268 AGSPLEFPVRKRLADSVLERKRISAABERKATKLGIIILCAFICQMPLPFYASLVLPIC    327
Qy     277 H-YIIPETLDVLIWFGLYNSTENPMVAFFEPWFERRALKMWL-FGKIF    323
Db     328 RDSQWMPGLEDFEFTWLGLYNLSLINPIITYVENEDFROAFORVLIHFRAKF    377

RESULT 13
SHID_HUMAN STANDARD; PRT; 377 AA.
AC P28221.
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 5-HYDROXYTRYPTAMINE 1D RECEPTOR (5-HT-ID) (SEROTONIN RECEPTOR)
DE (5-HT-ID-ALPHA).
DE HTRID OR HTRIDA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91342595; PubMed=1652050;
RA Hamblin M.W., Metcalf M.A.;
RT "Primary structure and functional characterization of a human 5-HTID-
RL type serotonin receptor."
RN Mol. Pharmacol. 40:143-148(1991).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92228840; PubMed=1565658;
RA Weinstein R.L., Zgombick J.M., Macchi M.J., Branchek T.A.,
RA Hartig P.R.;
RT "Human serotonin 1D receptor is encoded by a subfamily of two
RL distinct genes: 5-HTID alpha and 5-HTID beta."
RN Proc. Natl. Acad. Sci. U.S.A. 89:3630-3634(1992)."
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL, M89955; AAA35491.1; -.
EMBL, M81589; AAA60315.1; -.

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QY 133 KNNILVICVNIFFISWPAVAFGMIFELNFKGAEIYKHHVCHGCGSVFESKTS-CV 191  
DB 146 RTAGHAAMIAVAWAISICISIPPLFMR-QATAHEM-----SDCLVNTSQTSTYT 196  
QY 192 LRFMTSFYIPGIMLCVYRIYLAKEQ-----ARLISDA----- 226  
DB 197 YSTGAFYIPISILLITLYGRIVYAARSRLINPPLSYGKRFTTAQLITGSAGSSLCSDNS 256  
QY 227 -----NQ-----KIQIGLEMKNGISQSKERRAVRTGLVNGVFLICMCPFTI 268  
DB 257 LHESHTHVGSPLFNVQVKKIADSLTERKRISAAREKATKTLGILLAFIICWLPFV 316  
QY 269 CTVMPE-----FLHYIIPPTINDVLIWFGYLNSTFNPVYAFYFPMFKALMFLGKI 322  
DB 317 VSLVLPICNDSCMIH-----PALFDFPTWGLGYNLSLINPVIYIVFNEDEFQARQVYH--- 369  
QY 323 FQKDS 327  
DB 370 FRKAS 374

RESULT 15  
H2R\_HUMAN STANDARD: PRT; 359 AA.  
AC P25021: Q14464;  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAY-1993 (Rel. 22, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HISTAMINE H2 RECEPTOR (H2R) (GASTRIC RECEPTOR 1).  
GN HRH2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=91337087; PubMed=1714721;  
RA Gantz I., Munzert G., Tashiro T., Schaeffer M., Wang L.-D.,  
RA DelValle J., Yamada T.;  
RL "Molecular cloning of the human histamine H2 receptor";  
RL Biochem. Biophys. Res. Commun. 178:1386-1392(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95275318; PubMed=7755641;  
RA Nishi T., Koike T., Oka T., Maeda M., Futai M.;  
RT "Identification of the promoter region of the human histamine H2-  
RL receptor gene.";  
RL Biochem. Biophys. Res. Commun. 210:616-623(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=99297624; PubMed=10371214;  
RA Murakami H., Sun-Wada G., Matsumoto M., Nishi T., Wada Y., Futai M.;  
RT "Human histamine H2 receptor gene: multiple transcription initiation  
and tissue-specific expressionl.";  
RL FEBS Lett. 451:327-331(1999).  
RN [4]  
RP SEQUENCE OF 4-351 FROM N.A., AND POLYMORPHISM.  
RC TISSUE=Brain;  
RX MEDLINE=96414531; PubMed=8817552;  
RA Orange P.R., Heath P.R., Wright S.R., Pearson R.C.A.;  
RT "Allelic variations of the human histamine H2 receptor gene.";  
RL NeuroReport 7:1293-1296(1996).  
RN [5]  
RP REVIEW.  
RX MEDLINE=98042107; PubMed=9374694;  
RA DelValle J., Gantz I.;  
RT "Novel insights into histamine H2 receptor biology.";  
RL Am. J. Physiol. 273:G987-G996(1997).  
CC -I- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC  
ACID SECRETION. ALSO APPEARS TO REGULATE GASTROINTESTINAL MOTILITY  
AND INTESTINAL SECRETION. POSSIBLE ROLE IN REGULATING CELL GROWTH

CC AND DIFFERENTIATION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY  
CC G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND, THROUGH A SEPARATE  
CC G PROTEIN-DEPENDENT MECHANISM, THE PHOSPHOLIPID/PROTEIN KINASE  
CC (PKC) SIGNALING PATHWAY (BY SIMILARITY).  
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -I- DISEASE: ANTAGONISTS FOR THIS RECEPTOR HAVE PROVEN TO BE EFFECTIVE  
CC THERAPY FOR ACID PEPTIC DISORDERS OF THE GASTROINTESTINAL TRACT.  
CC CERTAIN ANTAGONISTS ARE USED IN THE TREATMENT OF NEUROPSYCHIATRIC  
CC AND NEUROLOGICAL DISEASES SUCH AS SCHIZOPHRENIA, ALZHEIMER'S  
CC DISEASE AND PARKINSON'S DISEASE.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL: M64799; AAA58647.1; -  
DR EMBL: D49783; BAA08618.1; -  
DR EMBL: AB023486; BAA84279.1; -  
DR EMBL: X98133; CAA66832.1; -  
DR PIR: JH0449; JH0449.  
DR GCRDB: GCR\_0176; -  
DR GCRDB: GCR\_1836; -  
DR GCRDB: GCR\_2080; -  
DR MIM: 142703; -  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
DR PRINTS: PR00531; HISTAMINEH2R.  
DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
FT DOMAIN 1 22  
FT TRANSMEM 23 44  
FT DOMAIN 45 57  
FT TRANSMEM 58 81  
FT DOMAIN 82 92  
FT TRANSMEM 93 114  
FT DOMAIN 115 134  
FT TRANSMEM 135 159  
FT DOMAIN 160 180  
FT TRANSMEM 181 204  
FT DOMAIN 205 234  
FT TRANSMEM 235 258  
FT DOMAIN 259 267  
FT TRANSMEM 268 289  
FT DOMAIN 290 359  
FT SITE 98 98  
FT SITE 186 186  
FT SITE 190 190  
FT CARBOHYD 4 4  
FT DISULFID 91 174  
FT VARIANT 217 217  
FT VARIANT 231 231  
FT VARIANT 268 268  
FT VARIANT 268 268  
FT CONFLICT 133 133  
FT CONFLICT 175 175  
FT CONFLICT 207 207  
SQ SEQUENCE 359 AA; 40098 MW; 9835AE2BA60B9B0F CRC64;

Query Match

26.2%; Score 472.5; DB 1; Length 359;



Best Local Similarity 32.68; Pred. No. 1.5e-23;  
Matches 106; Conservative 64; Mismatches 124; Indels 31; Gaps 5;

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QY 18 SNDVRASLYSLMVLILTLVGNLIVISISHFQOLHTPTNMLIHSMTVDLGLGLMP 77
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 14 STACKITTVLAVLILITVAGNVVCLAVGLNRRLNRLNCFIVSLAITDGLGLVLP 73

QY 78 YSAVSAEHCWYFGEVFCCKIHTSDIMLSASIFHLSPISIDRYAVCDPLRYKAKMNL 137
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 FSAIYQLSCCKMSFGKVCNITSLDVMCTASINLLEMISIDRYCAVMDPLRYPLVTPV 133

QY 138 VICVMIFISMSVPAVFAFGMITFLELNFKGAEEIYKHVHCRGGSVFPSKISGVLTEMTS 197
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 RVAISLVLIWVISITLSFLSIHLGWSNRHETS---KGNHTTSKCKVQVNEVYGLVDGLVT 190

QY 198 FYIPGIMLCVYRIRYIAKQOARLISDANQKLGLEMKNGISQSK-----ERKAVKTL 252
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 FYLPLLMCITYYRIFFKVARDOAKRI-----NHISWKAATIREHKATVTL 236

QY 253 GIVNGVFLICWCPFFICTVM-----DPLHAYIIPPTLNDVLIWFGYLNSTFNPWYAFYY 307
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 AAVMGAFILICWFPYFTAFVYRGLRGDDAINEV---LEAIYLMGLYANSALNPILYALN 292

QY 308 PWRRALKMMLFGKIFOKDSSRCKL 332
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 RDFRTGYOOLFCRLANRNSHKTSL 317
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Search completed: December 11, 2001, 16:10:45  
Job time: 121 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 11, 2001, 16:07:43 ; Search time 12.59 Seconds  
(without alignments)  
604.139 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801  
Sequence: 1 MPFCHNIINISCVKNMNSND.....FGKIFOKDSSRCKLFLELSS 338

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	813.5	45.2	343	2	US-08-788-539A-2
2	782	43.4	338	3	US-09-286-805-4
3	743	41.3	348	3	US-09-286-805-2
4	677.5	37.6	337	2	US-08-467-559B-2
5	534	29.7	388	1	US-08-446-822-8
6	529	29.4	387	1	PCT-US93-12586-8
7	529	29.4	387	1	US-07-996-772A-2
8	529	29.4	387	1	US-08-446-822-2
9	529	29.4	387	5	PCT-US93-12586-2
10	527	29.3	406	1	US-07-996-772A-4
11	527	29.3	406	1	US-08-446-822-4
12	527	29.3	406	5	PCT-US93-12586-4
13	486	27.0	358	2	US-08-748-485-6
14	478.5	26.6	376	1	US-07-817-920-5
15	478.5	26.6	376	1	US-08-117-006-5
16	478.5	26.6	376	1	US-08-216-594-5
17	478.5	26.6	376	5	PCT-US93-00149-5
18	477.5	26.5	375	1	US-08-370-542-5
19	477.5	26.5	375	1	US-08-542-358-5
20	477.5	26.5	375	3	US-09-018-351-5
21	474.5	26.3	359	3	US-08-875-540-15
22	474	26.3	377	2	US-08-461-812-2
23	474	26.3	377	2	US-08-157-185-14
24	474	26.3	377	3	US-08-281-526B-14
25	472.5	26.2	359	2	US-08-467-568-13
26	472.5	26.2	359	2	US-08-748-485-4
27	472.5	26.2	359	2	US-08-103-170-2

28	472.5	26.2	359	2	US-09-030-562-13	Sequence 13, Appl
29	461.5	25.6	348	3	US-08-875-540-13	Sequence 13, Appl
30	459.5	25.5	359	2	US-08-748-485-5	Sequence 5, Appl1
31	458	25.4	446	1	US-07-626-618A-21	Sequence 21, Appl
32	458	25.4	446	1	US-08-333-977-21	Sequence 21, Appl
33	456	25.3	446	2	US-07-969-267B-4	Sequence 7, Appl1
34	455	25.3	483	1	US-08-194-338-7	Sequence 7, Appl1
35	454.5	25.2	477	1	US-07-791-936A-2	Sequence 2, Appl1
36	454.5	25.2	477	1	US-08-383-781B-2	Sequence 2, Appl1
37	454.5	25.2	477	2	US-07-969-267B-2	Sequence 2, Appl1
38	452	25.1	417	5	PCT-US91-00909-2	Sequence 2, Appl1
39	452	25.1	418	1	US-08-194-338-9	Sequence 9, Appl1
40	452	25.1	418	3	US-08-817-869-12	Sequence 12, Appl1
41	450.5	25.0	359	2	US-07-996-772A-10	Sequence 10, Appl1
42	450.5	25.0	359	2	US-08-748-485-3	Sequence 3, Appl1
43	450	25.0	475	1	US-07-666-591-4	Sequence 4, Appl1
44	450	25.0	475	1	US-07-970-715-4	Sequence 4, Appl1
45	449.5	25.0	446	1	US-07-626-618A-22	Sequence 22, Appl1

## ALIGNMENTS

RESULT 1  
US-08-788-539A-2  
: Sequence 2, Application US/08788539A  
: Patent No. 5871967  
: GENERAL INFORMATION:  
: APPLICANT: SmithKline Beecham Corporation  
: TITLE OF INVENTION: CLONING OF A NOVEL G-PROTEIN  
: NUMBER OF SEQUENCES: 2  
: CORRESPONDENCE ADDRESS:  
: STREET: 709 Swedeland Road  
: CITY: King of Prussia  
: STATE: PA  
: COUNTRY: USA  
: ZIP: 19406  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/788,539A  
: FILING DATE: 24-JAN-1997  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Han, William T  
: REGISTRATION NUMBER: 34,344  
: REFERENCE/DOCKET NUMBER: ATG50047  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 610-270-5219  
: TELEFAX: 610-270-4026  
: TELEX:  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 343 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-788-539A-2

Query Match 45.2% Score 813.5; DB 2: Compugen 343;  
Best Local Similarity 46.0%; Pred. No. 1.9e-63;  
Matches 159; Conservative 57; Mismatches 99; Gaps 5;



```

? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: STEEFE, ERIC K
? REGISTRATION NUMBER: 36,688
? REFERENCE/DOCKET NUMBER: 1488, 08400000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 337 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-467-559B-2

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Query Match	37.6%	Score 677.5	DB 2	Length 337
Best Local Similarity	39.0%	Pred. No. 1.2e-51		
Matches 130; Conservative	67	Mismatches 125;	Indels 11;	Gaps 4;

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QY 3 FCHHIIINISCKNNKMSNDIVRASISLWVLIILTLTVLNVLIYVISHFQLOHPHTNMLIH 62
Dh 16 FCYO-VNGSCRRHTHTGICLOLVITLFCOAGMLIIVLGNVFAFVAFYSFKALHPHTNELL 74
QY 63 SMATVDFLLGLVMPYSWVNRBAEHCWYFGEFECIKHSTIDIMLSASIFHLSFSDIRY 122
Dh 75 SLADMFELGLVTLPLSTIKRSVESCEGFDGLCHHTLVLDLFCULTIFHLCISIDRHC 134
QY 123 AVCDDPLRYKAMNIIIVICMIFISWSVPAVAFQCMIFLELNFKAEBEYVKKVHVRGCS 182
Dh 135 AICDPLTPRSKFETVRVALRYTLAAGVPAATSTLELTVDVETRLSQ-WLEEMPCVSCQ 193
QY 183 VEFKISGVLFEMHSFYIPGSIIMCVYYRYIILINKEQARLISDANKLOIGLEBKNNISQ 242
Dh 194 LLLKFMWMLNF-PLFVPCILMISLVYKIRFVATROAQOITTLTKSL-----AGAA 244
QY 243 SKERRAVTLLGIVNGVPLICSCPEFICTVMDPRLHYIIPRLYNDVLLMFGULSTENPMY 302
Dh 245 KHERKAATLTGIVGYILICWLPRTPIIMVDSLLHFTIRPLVDFILMPAVFNACAPII 304
QY 303 YAFETYPWRKALMMLEGGIKITQKSSCKCLE 335
Dh 305 YVESIOWERRKALKLTLISOKVESPOTRVDYIOE 337

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RESULT 5  
 ; Sequence 8, Application US/08446822  
 ; Patent No. 5766879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SYNATIC PHARMACEUTICAL CORPORATION  
 ; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS  
 ; TITLE OF INVENTION: AND USUS THEREOF  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: COOPER & DUNHAM  
 ; STREET: 30 ROCKEFELLER PLAZA  
 ; CITY: NEW YORK  
 ; STATE: NEW YORK  
 ; ZIP: 10112  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/446,822  
 ; FILING DATE: June 1, 1995  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, P., John  
 ; REGISTRATION NUMBER: 28,678

```

? REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPM/MA
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 388 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-446-822-8

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Query Match	29.7%	Score 534;	DB 1;	length 388;
Best Local Similarity	37.4%	Pred. No.	4.4e-39;	
Matches 116;	Conservative 53;	Mismatches 121;	Indels 20;	Gaps 5

Qy	25	LYSAMVLITLTLGNLIVIVISYSHFQOLH-TPTNNMLIHSMAVDFLGLCIVMPYSVRS	83
Db	22	LTLFLSVIITLAILGNLNLVMAVCMQOLRKIKNTYFLISLAFNDLLVSLVMPFGAIEL	81
Qy	84	AELHCWYGEVFCFTHSTDLMLSSASIFPHLSFISIDRYAV-CDPLRYAKAKNITLVCM	142
Db	82	VQDITMIVGEVFCVLTSTIDVLTTLTASIFHLCCISLDRIYALICDPLRYAKNMPRLRLALM	141
Qy	143	IFISMSVPAVAFEGMIFLELNFKAEEIYYKHHVHCRCG---CSVFESKISGLVTPTMTSF	198
Db	142	LGGGMVPIPTFISFLPIMGOMNNIGIIDLEKRFKNQNSNSTYCVCFVNNKPYALICSVAF	201
Qy	199	YIPDSIMLCVYRITLYLAKEDARLISDANQKLQIGLEMKNGISG-----KERRA	248
Db	202	YIPLFLVNLAVIYRIVYAKKEHAHOI---QMLQAGASSSESRSPOSDOHSTHRRMTETKA	257
Qy	249	VKITLGIWGYELLICMCEFFLITVNDPFLHYLIIPPTLNDVLIWEGIINSTENPNVYAEFP	308
Db	258	AKTLICITINGCGCLCMADPEFVYINVIDPFIYDVPGQVMTAFILMGIYRSGINPFLYAFLNK	314
Qy	309	WFRKALKKML	318
Db	318	SERRAFLLI	327

RESULT 6  
PCT-US93/12586-8  
Sequence 8, Application PC/TUS9312586  
GENERAL INFORMATION:  
APPLICANT: SYMATIC PHARMACEUTICAL CORPORATION  
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM  
STREET: 30 ROCKEFELLER PLAZA  
CITY: NEW YORK  
STATE: NEW YORK  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12586  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, P., John  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPM/TEP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-12586-8

Query Match 29.7%; Score 534; DB 5; Length 388;  
Best Local Similarity 37.4%; Pred. No. 4,4e-39;  
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSIMALLITLVGNLYIVISISHKOLH-PTNNLIHSMATVDLLGCVMPYMSVRS 83  
DB 22 LTFEFTVITLMAILGNLWVAACWDRDLKIKTNFVLSLADLLSVLVNAFGAIEL 81  
QY 84 AEHCWYGEVEFCIKHTSTDIMLSSASIFHLFSIDRYAV-CDPLRYKAKNMLIYCV 142  
DB 82 VQDIWYGEVFLVRLSDVLTFTASIFHLCCISLDRYAICCPPLVYRKMTPLIALM 141  
QY 143 IFTSMVPAVFAFGMIFELNFKAGEIYKHYHCRG---CSVEFSKISGVLTMTSF 198  
DB 142 LGGCWVTFPISEFLPIMGNNIGIIDLIEKRKNQNSNTYCFVWVWVNAFGAIEL 201  
QY 199 YIFGSMILCVYRYIYLAKEQARLISDANKQIDGLEMNGISQ-----KERK 248  
DB 202 YIFPLMLAVIYRYIYTAEEHAQI---OMLQACASSERPSQADOSHTRMRTET 257  
QY 249 VTLGIVMGVFLICMCPFCICTVMDPEFLHYIIPPLNDVLMFGYLNSTFNPVAF 308  
DB 258 AATLCITMGCFCLGCAAFVFTVNIYDPFIDYTVPGQWTFAMLGYSINSLNPLV 317  
QY 309 WFRKALKMML 318  
DB 318 SERRAFLIIL 327

RESULT 7

US-07-996-772A-2  
Sequence 2, Application US/07996772A  
Patent No. 5472866  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe  
APPLICANT: Hartig, Paul R.  
APPLICANT: Branchek, Theresa A.  
APPLICANT: Weinsbank, Richard L.  
TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM  
STREET: 30 ROCKEFELLER PLAZA  
CITY: NEW YORK  
STATE: NEW YORK  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/996,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, P., John  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 42667/JPM/TEP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 387 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-996-772A-2

Query Match 29.4%; Score 529; DB 1; Length 387;  
Best Local Similarity 35.4%; Pred. No. 1.2e-38;  
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSIMALLITLVGNLYIVISISHKOLH-PTNNLIHSMATVDLLGCVMPYMSVRS 83  
DB 22 LTFEFTVITLMAILGNLWVAACWDRDLKIKTNFVLSLADLLSVLVNAFGAIEL 81  
QY 84 AEHCWYGEVEFCIKHTSTDIMLSSASIFHLFSIDRYAV-CDPLRYKAKNMLIYCV 142  
DB 82 VQDIWYGEVFLVRLSDVLTFTASIFHLCCISLDRYAICCPPLVYRKMTPLIALM 141  
QY 143 IFTSMVPAVFAFGMIFELNFKAGEIY---YKHVHCRGCSVEFSKISGVLTMTSF 198  
DB 142 LGGCWVTFPISEFLPIMGNNIGIYDIEKRKNHNSNTFCVWVWVNAFGAIEL 201  
QY 199 YIFGSMILCVYRYIYLAKEQARLISDANKQIDGLEMNGISQ-----244  
DB 202 YIFPLMLAVIYRYIYTAEEHA-----QOIQM-LQACASSERPSQADOSHTRMRT 253  
QY 245 ERKAVTGLIVMGVFLICMCPFCICTVMDPEFLHYIIPPLNDVLMFGYLNSTFNPV 304  
DB 254 ETKAATLIVMGCFCLGCAAFVFTVNIYDPFIDYTVPEKWTAFMLGYSINSLNPL 313  
QY 305 FEPYMERKALKMML 318  
DB 314 FLNKSERRAFLIIL 327

RESULT 8

US-08-446-822-2  
Sequence 2, Application US/08446822  
Patent No. 5766879  
GENERAL INFORMATION:  
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION  
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM  
STREET: 30 ROCKEFELLER PLAZA  
CITY: NEW YORK  
STATE: NEW YORK  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,822  
FILING DATE: June 1, 1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: White, P., John  
REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPM/MAT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 387 amino acids  
TYPE: amino acid



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Query Match          29.3%; Score 527; DB 1; Length 406;
Best Local Similarity 35.0%; Pred. No.1.9e-38;
Matches 110; Conservative 62; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSIMLVLIITLTVGNLIVYISHSFKQLH-TPTNMLIHSMAVFDVLGGCLVMPYSMVS 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 LITFPAVYIAMAIIIGNLVMAVAVCDROLRKIKTNVFIYSLAFADLLVSLVNAFGAIEL 81
QY 84 AEHCAYFEVEVEKIFITSDIMLSASISIFLSTISIDRIYAV-CDPLRKAKNNILVICYM 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 VODIMEFYEMECFLVTSIDVLLTTSISIFHLCLSLDRYYAIIACOPLVYFNKMTPIRIALM 141
QY 143 IIFISVAVAFVAFGNIPIELNFKGAETI---YKHVHCRGGSVFEFSISGLVFMTSE 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 LGGCVIIVMEFISFLIMOGMNNIGIVDYIEKKFNHNSSTFCVEMVNAKPIAITSVAE 201
QY 199 YIPSGIMLCVYRYIILAKEQARLISDANQKLOIGLEMKNGISQSK----- 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YIPFLIMLVAYRYIVTAKENH-----QQIQM-LQAGATSESNPQADGHSIHRMT 253
QY 245 ERKAKITGLIYWGAVVLLICMCPFFICTWADPFLHIILPPLNDVLIIMFGILNSTENPMYVA 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 EFKAKTKLCVIMGCFCFQWAPFVTVNIIDPFDYIVPEKVTAFMLGLGINSGLNDFIYA 313
QY 305 FEYPMFRKALKMML 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 FLNKSFRRAFLIIL 327

RESULT 11
US-08-446-822-4
: Sequence 4, Application US/08446822
: Patent No. 5766879
: GENERAL INFORMATION:
: APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
: TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: COOPER & DUNHAM
: STREET: 30 ROCKEFELLER PLAZA
: CITY: NEW YORK
: STATE: NEW YORK
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446,822
: FILING DATE: June 1, 1995
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: White, P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPM/MAT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-446-822-4

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OY 25 LYSMLAVLIITLTGVLNGLIVYSISHFQKOLH-TPTMWLIHSMATVPFLGCLVMPYSMVS 83
Db 22 LTTFPAWVILMALICNLNLMVAVACDRQRLRIKRTNFEVLSLAFADLLVSLVNAFGAIEL 81
OY 84 AEHCWYFGEVFECKINTSTDIMLSASISIFLPSISIDRYAAV-CDDPLRYKAKNIIVTCVA 142
Db 82 VQDIWFYFGMFCPLVTSIDVLTLTTSISIFLCCSLSDRYAALCCPLVYKNNKTPRLRIAM 141
OY 143 IFISNSVPAVFAFGMIFLELNFKADEIY---YKHVHCRCGCSVFFSKISCVLTFMISF 198
Db 142 LGGCVAIVIMFISFLDIMOGMWNIGIVDVIEKRKFNNHNSNSTFCVMVNNKPAITCSVVA 201
OY 199 YIPGSMICVYRYRIILKEQARLISDANQKIOIGLEMNGISOSK----- 244
Db 202 YIPELMLVATRYIVYTAKEHA-----QOLIM-LQAGATSESPQOTADOSHTRMRT 253
OY 245 ERKAVKTAGIYGVGLICMCPEFICTVMDPFLHYIIPPLINDVLIMFGVLTSTFNPMYVA 304
Db 254 ETKAKTLCVIMGCPCFCPCAFPEFVGINVDPLFDIYVPEKVMAPFLMIGVLTGSLNPELVA 313
OY 305 PFYWFERKALKMML 318
Db 314 FLNKSFRRAFLIIL 327

RESULT 12
PCT-US93-12586-4
: Sequence 4, Application PC/TUS9312586
: GENERAL INFORMATION:
: APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
: TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESSES:
: ADDRESSSEE: COOPER & DUNHAM
: STREET: 30 ROCKEFELLER PLAZA
: CITY: NEW YORK
: STATE: NEW YORK
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/12586
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPM/TEP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
: TELEEX: 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US93-12586-4

Query Match 29.3%, Score 527, DB 5, Length 406;
Best Local Similarity 35.0%, Pred. No. 1,9e-38, 1.4%
Matches 110; Conservative 62; Mismatches 114; Indels 28; Gaps 6.

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IMMEDIATE SOURCE:  
CLONE: 5-HT1DA  
US-07-817-920-5

Query Match 26.6%; Score 478.5; DB 1; Length 376;  
Best Local Similarity 34.0%; Pred. No. 2.9e-34;  
Matches 122; Conservative 55; Mismatches 111; Indels 71; Gaps 11;

QY 21 VRASLSLNAVLIITLVGNLIYVSIHFKQLHTPTNMLHSMATVDELGLGVMPYSN 80  
DB 37 LKISLPEVLLSVITLATVLSNAFVLTITLLTRKLTNPANLYLSLATDVLVSLVMPISM 96  
QY 81 VRSAEHCWYEGEVCKIHTSTDIMLSASIFHLSPFISIDRYAVCPDLYKAKMNIIVIC 140  
DB 97 ATTITHTWNEGQILCDIMWSSDITCTCTASTILHCVIALDRYAITALEYSKRRTAGHAA 156  
QY 141 VMIFISVPAVAFAGMIFLEINFKGADEIYYKHVHCRGCSVFESKIS-GVLTFTMTSEY 199  
DB 157 TMAIYMAISICISIPPLFWROE-KAQEEM-----SDCLVNTSQISYIYSTGCAFY 207  
QY 200 IFGSIMLCYRRILYLAKEO-----ARLIDA-----NOKLOIG----- 233  
DB 208 IPSVLLIILYGRILYRAARNRILNPPLSGKRFTTAHLITGSAGSVCSLSLSHEGSHSA 267  
QY 234 -----LEMKNGISOSKERKAVKTGIWGVFLICWCPFFICTVMDP-- 274  
DB 268 GSPLEFNHVKIKLADSALEKRR-ISAAREKAKIKIIGIILGAFIICWLPFFVSVLPIC 326  
QY 275 ---FLHYIIPPTLNDVLIWFGYLNSTFNPVYAFEPYPMFRKALKMMLEFKI--FOKDS 327  
DB 327 RDCSWIH----PGLFDFFTWLGYNLSLNPDIITYVNEERQA-----FOKIVPFRKAS 376

RESULT 15  
US-08-117-006-5  
Sequence 5, Application US/08117006  
Patent No. 5639652

GENERAL INFORMATION:

APPLICANT: Weinshank, Richard L.  
APPLICANT: Branchek, Theresa  
TITLE OF INVENTION: DATA ENCODING A HUMAN 5-HT1F RECEPTOR AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect, Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,006

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/39318  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
IMMEDIATE SOURCE:  
CLONE: 5-HT1DA  
US-08-117-006-5

Query Match 26.6%; Score 478.5; DB 1; Length 376;  
Best Local Similarity 34.0%; Pred. No. 2.9e-34;  
Matches 122; Conservative 55; Mismatches 111; Indels 71; Gaps 11;

QY 21 VRASLSLNAVLIITLVGNLIYVSIHFKQLHTPTNMLHSMATVDELGLGVMPYSN 80  
DB 37 LKISLPEVLLSVITLATVLSNAFVLTITLLTRKLTNPANLYLSLATDVLVSLVMPISM 96  
QY 81 VRSAEHCWYEGEVCKIHTSTDIMLSASIFHLSPFISIDRYAVCPDLYKAKMNIIVIC 140  
DB 97 ATTITHTWNEGQILCDIMWSSDITCTCTASTILHCVIALDRYAITALEYSKRRTAGHAA 156  
QY 141 VMIFISVPAVAFAGMIFLEINFKGADEIYYKHVHCRGCSVFESKIS-GVLTFTMTSEY 199  
DB 157 TMAIYMAISICISIPPLFWROE-KAQEEM-----SDCLVNTSQISYIYSTGCAFY 207  
QY 200 IFGSIMLCYRRILYLAKEO-----ARLIDA-----NOKLOIG----- 233  
DB 208 IPSVLLIILYGRILYRAARNRILNPPLSGKRFTTAHLITGSAGSVCSLSLSHEGSHSA 267  
QY 234 -----LEMKNGISOSKERKAVKTGIWGVFLICWCPFFICTVMDP-- 274  
DB 268 GSPLEFNHVKIKLADSALEKRR-ISAAREKAKIKIIGIILGAFIICWLPFFVSVLPIC 326  
QY 275 ---FLHYIIPPTLNDVLIWFGYLNSTFNPVYAFEPYPMFRKALKMMLEFKI--FOKDS 327  
DB 327 RDCSWIH----PGLFDFFTWLGYNLSLNPDIITYVNEERQA-----FOKIVPFRKAS 376

Search completed: December 11, 2001, 16:08:59  
Job time: 76 sec

10/10/01

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10/10/01

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